STIC-Biotech/ChemLib

86128

Fr m: Sent:

Bunner, Bridget Thursday, February 06, 2003 11:54 AM STIC-Biotech/ChemLib sequence search

To:

Subject:

Hi! I'd like a sequence search performed for case 09/762,594:

1. the nucleic acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

Art Unit 1647 CM1-10D12 (703) 308-7148 mailbox 10B19

Point of Contact: Susan Hanley Technical Info. Specialist CM1 6B05 Tel: 305-4053

| Searcher: |
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| Phone: |
| Location: |
| Date Picked Up: |
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| TYPE OF SEARCH: |
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| Description | PBR-associated pro Human polynucleoti | Human NTAP cDNA cl Human polynucleoti | Human secreted pro Human ORFX ORF2918 | Murine transport a Human ORFX ORF3021 | DNA encoding human |
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| SUMMARIES | AAZ57038 AAK52051 | AAZ87207 AAK53035 | AAA93116 AAC77363 | AAK53762 AAC77466 | ABK24346 |
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| cervic | n immune/ | | Human foetal liver | Human brain expres | Human bone marrow | Probe #7921 for ge | Probe #11664 used | Human genome-deriv | Human foetal liver | Human brain expres | Human bone marrow | Probe #18080 for g | Probe #25870 used | Human genome-deriv | Drosophila melanog | Human prostate exp | Human cervical can | Polyglutamine trac | Human prostate exp | Mannose-1-phosphat | Kaposi's sarcoma-a | Nucleotide sequenc | Kaposi's sarcoma-a | KSHV LUR DNA (nucl | KSHV long unique c | DNA | | DNA encoding novel | e LOBO | FLGA insert stabil | Nucleotide sequenc | Epstein Barr virus | EBV tethering prot | Nucleotide sequenc | Epstein-Barr virus | |
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BP.

Peripheral-type benzodiazepine receptor; PBR; PBR- associated protein; PAP; cell proliferation; cancer; cell death; cytostatic; neuroprotective; immunomodulator; antiinfertility; cerebroprotective; atherosclerosis; Niemann-Pick C; tumour; Alzheimer's disease; developmental disorder; cholesterol; multiple sclerosis; stress; neurodegenerative disorder; immune disorder; stroke; PAP7; ss. PBR-associated protein (PAP)7 encoding cDNA Location/Qualifiers 8..1399 /product= "PAP7" 99WO-US18507 (first entry) /*tag= WO200009549-A2. 11-AUG-1999; 19-MAY-2000 24 - FEB - 2000 ds snw Key

98US-0096048

11-AUG-1998;

ACGGGAGGAGGAGGAGGCGGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAGCAAAA 540

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The invention provides isolated peripheral-type benzodiazepine receptor (PBR) associated proteins (PAPS) and nucleic acids encoding the PAP proteins. The PAP polynucleotides are a source of primers and probes for detection, isolation and amplification. PAP ligands or substrates or antibodies can be labeled and used to detect PAPS, in the diagnosis and prognosis of disease associated with increased cell proliferation, such as cancer, or reduced cell death. The diagnostic methods of the invention can be predictive of diseases involving PBR including control invention. Schyder's corneal crystalline dystrophy, brain disorders including Alzhaimer's disease, cholesterol metabolism, control abnormalities, demyelinization, charcot-Marie tooth disease, Pelizaeus-Merzbacher disease, Multiple sclerosis, and SLA. The compounds effective in prophylactic treatments, or in screening correct intention in prophylactic treatments, or in screening correct disease. Which modulate PBR activity. Inhibitors of PAPP may be consed in the treatment or amelioration of conditions such as stress and stroke, cancer, neurodegenerative disorders, developmental disorders, conference infertility and immune disorders. The present sequence represents a cDNA
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(GEOU ) UNIV GEORGETOWN MEDICAL CENT
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                                                                                                                                               Novel peripheral-type
for the regulation of
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                                        Papadopoulos V,
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Length 1459; Sequence 1459 BP; 455 A; 298 C; 403 G; 303 T; 0 other; 21; DB 100.0%; Score 1459; 100.0%; Pred. No. 0;

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AAK52051 standard; cDNA;

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RESULT

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                                                                           therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAAAAAGATGGCAAAGCATTTCATCCAACTTATGAAGAAAAATTGAAGCTTGTGGCACT 356
                                                                                                                                                                                                                                                                                                                                                                                Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to polynucleotides (AAK51456-AAK53435) and the
                                                                       Human; cytokine; cell proliferation; cell differentiation; gene th
waccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCATAAGCAAGTTCTTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and (AAM80020) are omitted as the relevant pages from the sequence lisere missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3399;
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Wang ?
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R,
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nng J, Ren F, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1079.6; DB 2: Pred. No. 5.5e-280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Zhang J, Ren
I, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Page 2141-2144; 6221pp; English.
                                                Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                             Drmanac RT,
Wang J, Zha
Wejhrman T,
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2000US-0508075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
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87.2%;
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                          (first entry)
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Wang D, V
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                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                      Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAM78918
                                                                                                                                                             WO200157190-A2
                                                                                                                                                                                                                                                27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                 15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammation.
                                                                                                                                      Homo sapiens
                                                                                                                                                                                                             05-FEB-2001;
                                                                                                                                                                                                                                      03-FEB-2000;
                        06-NOV-2001
AAK52051;
                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
Zhao QA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAZ87205-Z87210 represent cDNAs encoding six human
neurotransmission-associated proteins (NTAPS, AAY77121-Y77126). The
present sequence, clone 998868, encodes a benzodiazepine
creceptor-associated frome human kidney tumour cDNA library. The NTAPS are
fragments isolated from a human kidney tumour cDNA library. The NTAPS are
used for treatment or prevention of neurological diseases (e.g.,
Alzheimer's, Parkinson's or Huntington's diseases, cerebral neoplasms, or
multiple sclerosis). They can also be used to raise specific antibodies
and to screen for specific binding agents (potential (agonists and
antosonists). NTAP-encoding nucleic acids are useful for recombinant
production of NTAPs, and as a source of therapeutic antagonists
(antisense, triplex-forming or ribozyme molecules). The nucleic acids may
also be used as a source of probes and primers for diagnosis or
cancing of NTAP expression in hybridisation/amplification tests, for
chromosome mapping and for identifying related sequences, and for gene
therapy. NTAP antagonists are used to treat and prevent a wide range of
cancers and immune disorders (e.g. AIDS, asthma, Crohn's disease,
             GAGGICCAAGICCGICIACIACAAGAGICIAITAIACIAGAIAGAGCIGCIGIICCAAGGI 1416
                                        GCGGTCAAAATCAGTCTACTACAGAGTCTATTATACTAGATAAAAATGTTGTTACAAAGT 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human neurotransmission associated proteins, useful for treatment, prevention and diagnosis of neurological disease, e.g. Alzheimer's disease, and antagonists for treating cancer or immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                             benzodiazepine receptor-associated protein; neurological disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; cerebral neoplasm; multiple sclerosis; drug screening; gene therapy; antagonist; cancer; AIDS; asthma; Crohn's disease; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human neurotransmission-associated (NTAP) 998868"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gorgone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guegler KJ,
                                                                    CCGGAGTCCAGGGTTGAGCACAACATGACGTTTAATTT 1454
                                                                                 Neurotransmission-associated protein; NTAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 65; 67pp; English.
                                                                                                                                                                    AAZ87207 standard; cDNA; 1481
                                                                                                                                                                                                                                                      Human NTAP cDNA clone 998868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US15121
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                                                                                                                                                                                                                            (first entry)
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/product=
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4R, Patterson
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P-PSDB; AAY77123.
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                                                                                                                                                                                                AAZ87207;
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                                     1557
                                                                   1417
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in
              detect NTAPs, for diagnosis or monitoring, as therapeutic antagonists, competitive drug screens, and for affinity purification of NTAPs from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 156
                                                                                                                                                                                                               GCATAAGCAAGTTCTTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT 216
                                                                                                                                                                                                                                                                                                                                                                                                           GGATGCCATGGTGGAGTTTGTCAAGCTCTTAAATAGGTGTTGCCATCTCTTTTCAACATA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGAAGGCAGCGTGAAGAGGAAGAACGAGGGGCTGCAAAAGGAAGAAGAAGAAGAAGGGAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGAAGGCGGCGTGAAGAGGAAGAAAAGACGTCTGCCAAAGGAGGAAGAAAACGTAG 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCATTGCCTGCATCATCAAAGGTGAACACAGCTGGAGCAAGTGATACACTGTCAGTTAA 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            730 TTCCTTGCCTACATCATCAAAAGTGAATGCAACTGTACCAAGTAATATGATGTCAGTTAA 789
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                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                          TGATGTGTTGGGGAATGATAGGAGGAGAGAATGGGCCAGCTCTGGGAAACATGTCCAAGGA
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                                                                                                                                                                                                                                                                                                     GCATAAGCAAGTTCTTATGGGCCCATATAATCCAGACACTTGTCCTGAGGTTGGATTCTT
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                                                                                                                        Score 1073.2; DB 21; Length 1481;
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0
                                                                                                                                                            Indels
                                                                                     Sequence 1481 BP; 467 A; 289 C; 403 G; 322 T; 0 other;
                                                                                                                                                            178;
                                                                                                                                            Pred. No. 1.9e-278;
                                                                                                                                                            Mismatches
osteoporosis, viral or other infections).
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                                                                                                                        73.6%;
86.9%;
                                                                                                                                                            Conservative
                                                                                                                                            Similarity
                                                      natural sources
                                                                                                                                                            Matches 1180;
                                                                                                                          Query Match
                                                                                                                                            Local
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useful in diagnosis and gene therapy
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GCGGTCAAAATCAGTCTACTACAGAGTCTATTATACTAGATAAAAATGTTGTTACTACAAAGT 1389
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                                                  CCACCAGTATCCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTG
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                                 CCTATTTTGGGAATTTGCCACAGACAGTTATGACATTGGGTTTGGGGTTTATTTTGAATG
                                                                                                   GACAGACTCTCCAAATGCTGCTGTCAGTGTGCATGTCAGTGAGTCCAGTGACGAGGAG
                                                                                                                                                                   GGAGGAGGAAGAAAATGTCACTTGTGAAGAAAAAGCAAAAAAGAACGCCAACAAGCCTCT
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F, C
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Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
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2000US-0598075.
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Wang D,
Yang Y, W
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20-JUN-2000;
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Zhao QA,
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to yetokine, cell proliferation or cell differentiation or which may induce production of other cytckines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or epetide therapy. The polypeptides have various cytckine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, insue growth factor activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                         2111 (AAK52582) and 3666 from the sequence listing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | GGATGCCATGGTAGAGTTTGTGAAGCTTCTAAATAAGTGTTGTCCTCTCCTCCTCGGCATA 336
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6221pp; English.
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Page 4841-4842;
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Matches 1177; Conserv
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nutritional supplement; immune modulation; autoimmune disorder;
haematopoiesis regulation; tissue growth; haemostasis; inflammation; ss.
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                                                                                                                         CGAGGAGGAAGAAGAAAACATCGGTTGTGAAGAGAAAGCCAAAAAGAATGCCAACAAGCC
                                                                                                                                                                        ATGGACAGACTCTCCAAATGCTGCTGTCAGTGTGCATGTCAGTGAGTCCAGTGACGAGGA
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                       GTGGACAAGACCACAAATCAAAGACTTTAAAGAGAAGATTCGGCAGGATGCAGATTCTGT
                                                                      TCTGCTGGATGAGATTGTACCTGTGTACCGGCGGGACTGTCACGAGGAAGTATATGCAGG
                                                                                                                                                                                                                                                                                                                   Human secreted protein coding sequence SEQ ID NO: 31
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                                                                                                                                                                                                                                              protein"
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The present sequence is the coding sequence for a human secreted protein. It was isolated from an adult pancreas cDNA library. The proteins and coding sequences of the invention can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have uses as nutritional supplements, as cytokine or cell proliferation factors, in immune modulation, where they may be used to treat immune and autoimmune diseases, as haematopoiesis regulators (treating myeloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, haemostatic or thrombolytic activity, or anti-inflammatory activity.
                                                                                                                                                                                                                                                                                                                                                                                           New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research, as well as nutritional sources or supplements -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGACCACAAATCAAAGACTTTAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGATTACA 1000
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                                                                                                                                                                                                                                                                                       Rapiejko
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                                                                                                                                                                                                                                                                                     Hall J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 40; Page 262-263; 309pp; English
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86.2%;
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99US-019633.
99US-0149639.
99US-0155686.
99US-0157247.
99US-0167822.
99US-0167823.
2000WO-US04340
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                                                                                                                                                                                                                                          (ALPH-) ALPHAGENE INC
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18-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                               Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antinflammatory; antidiabetic; hypothyroidism; SCID; AIDS; severe combined immunodefictency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; broom damage; cartilage damage; antilinflammatory disease; coagulation;
                                                                                                                                                CAGTATCCAGGGAGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTGGAGG 1360
                    1121 GACTCTCCAAATGCTGCTGTCAGTGTGAGTGAGTGAGTCCAGTGACGAGGAGGAGGAG 1180
                                                             GAGGAAGAAAATGTCACTTGTGAAGAAAAAGCAAAAAAGAACGCCCAACAAGCCTCTGCTG 1240
                                                                                                                                                                                           601
                                                                                                                                                                      721
                                                                                                                             661
                                                                                                                                                                                                      422 TTTTGGGAATTTGCCACAGACAATTATGACATTGGGTTTGGGGTGTATTTTGAATGGACA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and peptides derived from open reading frame X,
                                                                         602 GATGAGATTGTGCCTGTGTGTACCGACGGGACTGTCATGAGGAGGTGTATGCTGGCAGCAT
                                                                                                                                                                     662 CAATAICCAGGGAGAGGTCTAICTCCTCAAGTTIGACAACTCCTACTCTTIGTGGCGG
                                                                                                                                                                                                                                                                                                                                                                             Human ORFX ORF2918 polynucleotide sequence SEQ ID NO:5835.
                                                                                                                                                                                                                                     AGTCCAGGGTTGAGCACAACATGACGTTTAATTT 1454
                                                                                                                                                                                                                                               AAC77363 standard; cDNA; 420 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombosis; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127607.
99US-0127636.
99US-0127728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-602362/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000;
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02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                        08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                   AAC77363;
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antipsoriatic, antiparkinsonian, notropic; neuroprotective; osteopathic; antiporulsant; antiarthric; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatchgical; immunosuppressant; antidiabetic; hypotensive; dermatchgical; immunosuppressant; antidiabetic; hypotensive; dermatchgical; immunosuppressant; antidiabetic; hypotensive; dermatchgical; antifungal; antirheumatic; antidiflammatory; antibacterial; antiviral; antifungal; antirheumatic; antidiflammatory; antibacterial; antiviral; antifungal; antirheumatic; antidiflammatory; antibacterial; antiviral; antichnegatic and encerged pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus carterial or fungal infection, malarial, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturial haemoglobinial, antiniflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine transport and binding associated protein encoding cDNA SEQ ID 327.
                                                                                                                                                                                               AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGGTTCGTGGCACT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGATGCCATGGTAGAGTTTGTGAAGCTTCTAAATAAGTGTTGTCCTCTCCTCTCGGCATA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGATGCCATGGTGGAGTTTGTCAAGCTCTTAAATAGGTGTTGCCATCTCTTTTCAACATA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine, liver; gene library; amino acid synthesis; binding protein; cell metabolism; energy metabolism; fatty acid metabolism; synthesis; phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide; replication; transcription; translation; transport protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATAAGCAAGTTCTTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coagulation; to inhibit thrombosis; and as a contraceptive
useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 293.2; DB 21; Length
Pred. No. 9.2e-69;
0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 420 BP; 134 A; 69 C; 127 G; 88 T; 2 other;
                                                                                                                         Claim 5; Page 5005; 5507pp; English.
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89.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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4atches 316;
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antiviral; antibacterial; antifungal;
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                                                                                                               Homo sapiens.
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                                                                                                                                                                                                               02-APR-1999;
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                                                                                                                                                                                                                          05-APR-1999;
                                                                                                                                                         05-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                        This invention describes a novel gene library (A) comprises a gene sequence (or its part) encoding a protein involved in amino acid synthesis, cellular/energy metabolism, metabolism of fatty acids/phospholipids, synthesis or breakdown of purines/pyrimidines/nucleosides/nucleotides, DNA replication/transcription/translation, or is a transport/binding protein. (A) are produced that correspond to the 3'-end of mRNA but without the polyA tail. They can be prepared more efficiently and with less effort than conventional libraries. AAK53436-AAK54275 represent fragments of the gene library described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                        Gene library containing sequences with specific 3'-ends and no polyA tail, encoding proteins involved in a wide range of cellular processes
                                                                                                                                                                                                                                                                                                                                                                                                                    1187 GAAAATGTCACTTGTGAAGAAAAAGCAAAAAGAACGCCAACAAGCCTCTGCTGGATGAG 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTCTGTGGAGGTCCAAG 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCGTCTACTACAGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTCCA 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                277 GAAAATGTCACTTGTGAAGAAAAAGCAAAAAAAGAACGCCAACAAGCACCTCTGCTGGATGAG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                         Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF3021 polynucleotide sequence SEQ ID NO:6041.
                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                   Sequence 278 BP; 69 A; 72 C; 58 G; 79 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4e-62;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTTGAGCACAACATGACGTTTAATTTCCTTT 1459
                                                                                                                                                                                                                                                                                                                                                                         Score 268.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 109; 251pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                         18.4%; 98.98; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC77466 standard; cDNA; 291
                                                                2001DE-2003510
                                                                                       99DE-1058160
                                                                                                            (LION-) LION BIOSCIENCE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 98.9
nes 270; Conservative
                                                                                                                                   WPI; 2001-368570/39
                     DE20103510-U1
Mus musculus.
                                                                 28-FEB-2001;
                                                                                       02-DEC-1999;
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Machine the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiportatic; antiportatic; immunosuppressant; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antithrough; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, candiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus crythmatosus, severe combined immunodeficiency (SCID), AIDS, viral, cancerial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, concurnal hememoglobinuria, antinflammatory disease; to enhance
antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 AGAGGAAAGGCTTCGACGGGAGGAAGAGGAAAGGAGGACGGATAGAAGAAGAAGAAGTTCG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526 GCTGGAACAGCAAAAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATT 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAGACCGGCTGAGACGGGAGGAGGAGGAGGCGGCGGCGGATAGAGGAAGAGAGGCTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for treating e.g. cancers, proliferative disordenerodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 291 BP; 105 A; 58 C; 88 G; 40 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 5226; 5507pp; English.
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87.1%;
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99US-0127636.
99US-0127728.
2000US-0540763.
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AAH72906 standard;
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14-MAR-2000;
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           12-MAY-2000;
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21-JUL-2000;
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                                                                                                                                                                            19-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Schlegel R,
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                                                                                                                                                     AAH72906;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAACGCCAACAAGCCTCTGCTGGATGAGATTGTACCTGTGTACCGGCGGGGACTGTCACG 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTCCAGTGACGAGGAGGAGGAGGAGGAAATGTCACTTGTGAAGAAAAAGCAAAAA 1217
3 AGGCCAGCGATGACGACGAGGAGGAAGAAGGAACATCGGTTGTGAAGAGAAAAGCCAAAA 62
                                    CCAGCAGTATGCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical compositions, such as vaccines, for treating or preventing lung cancer, or as probes or primers for nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Switzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 934 BP; 272 A; 176 C; 206 G; 274 T; 6 other;
                                                                                                                                                                                                                                   33
                                                                                                                                                                                                                                  DNA encoding human lung cancer protein, Seg ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotides,
                                                                                                                                                                                                                                                         Human; lung cancer; cytostatic; vaccine; gene; ss
                                                                               CCAGCTGCAGGAGCACCACTATCAGCAGTATAAACACCAG 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 204.4; DB 2.
Pred. No. 1.1e-44;
2; Mismatches 43
                                                                                            243 CCAGTTGCAGGAGCAACATTCAGCAGTACATGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                  Klee JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer coding sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 138; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New lung tumour polypeptides and
                                                                                                                                                                 BP.
                                                                                                                                                              ABK24346 standard; cDNA; 934
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84.2%;
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2000US-230475P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hybridisation
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06-SEP-2000;
                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated nucleic acid for diagnosing and treating cervical cancer for assessing and detecting compounds for treating the cancer
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                                                     TAGAGCTGCTGTTCCAAGGTCCGGAGTCCAGGGTTGAGCACAACATGACGTTTAATTT 1454
182 GACAACTCCTACTCTTTGTGGCGGTCAAAATCAGTCTACTACTACTATTATATACTAGA
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Pred. No. 4.5e-28;
0; Mismatches 29; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                       Human cervical cancer marker nucleic acid 4180
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                                                                                                                                                                                                                                  BP.
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nilarity 84.7%; P
Conservative 0;
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99US-0171350.
2000US-0189315.
2000US-0203791.
2000US-0220114.
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2000US-0231968
2000US-0232397
2000US-0232399
2000US-0232400
2000US-0232400
2000US-0233064
2000US-0233064
2000US-0233064
2000US-0234064
2000US-0234064
2000US-0234064
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2000US-0236368.
2000US-0236369.
2000US-0236370.
2000US-0236802.
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2000US-0237040.
2000US-0239935.
2000US-0239937.
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2000US-0241221.
2000US-0241785.
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2000US-0244617.
2000US-0246474.
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2000US-0246477.
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2000US-0246527
2000US-0246528
2000US-02466528
2000US-0246610
2000US-0246611
2000US-0246611
2000US-0246613
2000US-0249208
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2000US-0235836.
2000US-0235327.
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2000US-0246524.
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2000US-0241808.
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2000US-0249264
               08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
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27-SEP-2000;
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7-NOV-2000;
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17-NOV-2000;
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                                                                                                                                                                                                                                                  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32183
                                                                                                                   AAK77371 standard; DNA; 4384 BP
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2000US-0217487
2000US-0218290
2000US-0220963
2000US-0220964
2000US-0224518
2000US-0224519
2000US-0224519
2000US-022514
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2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-021886.
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2000US-0189874
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                   433 GACCAAAAG 441
894 GACCAAAAG 902
                                                                                                                                                                                                                                                                                                                                          WO200157182-A2
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04-FEB-2000;
02-MAR-2000;
16-MAR-2000;
11-MAR-2000;
18-APR-2000;
19-APR-2000;
19-APR-2000;
10-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
26-JUL-2000;
14-JUL-2000;
26-JUL-2000;
14-JUL-2000;
26-JUL-2000;
14-JUL-2000;
14-JUL-2000;
16-JUL-2000;
16-JU
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
30-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-2001;
                                                                                                                                                                                      07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                     AAK77371;
                                                                                    RESULT 11
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Seq ID No 32.

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foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel human lung cancer polynucleotide (I) and polypeptides (II). (I) and (II) are useful in pharmaceutical compositions, such as vaccines, for the diagnosis and treatment of lung cancer. The polynucleotides are also useful as probes or primers for nucleic acid hybridisation. ABK24314-ABK24397 represent human lung cancer coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1305 ATCCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTGGAGGTCCA 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTCCGTCTACTACAGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTC 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AATCAGTCTACTACAGAGTCTATTATACTAGATAAAAATGTNGGTACAAAGTCTGGAGTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATCCAGGGAGAGGAGTCTATCTCCTCAAGNTTGACAACTCCTACTCTTTGTGGCGGNCAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New lung tumour polypeptides and polynucleotides, useful in
pharmaceutical compositions, such as vaccines, for treating or
preventing lung cancer, or as probes or primers for nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 113.4; DB 24; Length 527;
Pred. No. 2.6e-20;
0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human foetal liver single exon nucleic acid probe #11260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 527 BP; 141 A; 103 C; 112 G; 160 T; 11 other;
                                                                                  Human; lung cancer; cytostatic; vaccine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                   Bangur CS, Klee JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1425 CAGGGTTGAGCACACATGACGTTTAATTT 1454
                                         DNA encoding human lung cancer protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TAGGGTTGGGCAGAAGATGACATTTAATTT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 138; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.8%;
84.0%;
                                                                                                                                                                                                                                                 25-MAY-2001; 2001WO-US17066.
                                                                                                                                                                                                                                                                                         26-MAY-2000; 2000US-207485P.
06-SEP-2000; 2000US-230475P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA62955/c
ID ABA62955 standard; DNA; 554
09-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-122068/16.
                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                   WO200192525-A2.
                                                                                                                                                                                                                                                                                                                                                                                                 Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2002
                                                                                                                            Homo sapiens
                                                                                                                                                                                                          06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA62955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
contracts on by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
consideration into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
confers and cancer metastases of haematopoietic-derived cells. AAK64703
confers and cancer metastases of haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK84950 and AAM82169
confersent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATAAGCAAGTICITITGGGCCCATATAACCCAGACACGTCCCCTGAGGTIGGATTCTT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 32183; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4384 BP; 1434 A; 933 C; 758 G; 1259 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 129; DB 22;
Pred. No. 4.5e-24;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 TGATGTTGGGGAATGATAGGAGGAGAATG 249
                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.8%;
90.2%;
                                                                                               2000US-0250391.
2000US-0251030.
2000US-0251988.
                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                      2000US-0251990.
2000US-0254097.
                                                                                                                                                                                                    2000US-0251856
2000US-0251868
                                                                                                                                                                                                                                               2000US-0251869
                                                                                                                                                                                                                                                                       2000US-0251989
                                                                                                                                                                                                                                                                                                                                  05-JAN-2001; 2001US-0259678
                                       2000US-0249299
                                                                                                                                                                 2000US-0256719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483426/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                             01-05C-2000;
05-08C-2000;
05-08C-2000;
06-08C-2000;
08-08C-2000;
08-08C-2000;
08-08C-2000;
08-08C-2000;
08-08C-2000;
                                                                                                                                                                                                                                                                                      08-DEC-2000;
11-DEC-2000;
                                       17-NOV-2000;
17-NOV-2000;
                                                                            01-DEC-2000;
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metastasis

Rosen CA,

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Gaps

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WO200157277-A2

09-AUG-2001

Homo sapiens

ABK24345 standard; cDNA; 527

ABK24345

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ABK24345;

Switzer A;

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Homo sapiens
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                                                                                                                                                                                                                                                                                   brains
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                                                                                                                                                                                                                                                                                 measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                961 TAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGATTACAGTACGTCGAGGAGAAGTCGT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021 CACCGTCCGAGTCCCGACTCATGAGGAAGGATCATACCTATTTTGGGAATTTGCCACAGA 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1081 CAGTTATGACATIGGGTTTGGGGTTTATTTTGAATGGACAGACTCTCCCAAATGCTGCTGT 1140
                                                                                                                                                                                                                                                                                                                  fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGACTCTCTTCCAGTGATTGCAGCTCCATCCATGTGGACAAGACCACAAATCAAAGACTT 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 AGTCTCCCCACCTCTGATGGCTCCTCCATGCATCTGGACCTTTGCCAAGGTGAAGGAATT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 TGACTATGACATTGGCTTTGGAGTTTATTTTGACTGGACCCCTGTAACTAGCACTGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 CAAAAGCAAGCTGGGCAAAGAAGAACAGCCGTCTGGTGGTGGAGCGTGGTGGT
                                                                                                                                                                                                           for
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 AACTGTGCAGGTCAGTGATTCCAGTGACGATGAGGATGAAGAAGAGGAAGAG 191
                                                                                                                                                                                                                                                                       probe for
                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver - \,
                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 11260; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 7.6%; Score 110.6; DB 22; Length 61.1%; Pred. No. 1.5e-19; ive 0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human brain expressed single exon probe SEQ ID NO: 11355
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 554 BP; 156 A; 149 C; 114 G; 135 T; 0 other;
                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid
                                                                                                                                                            DR;
                                                                                                                                                            Rank
                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                           Hanzel DK, Chen W,
                                               2000US-0207456.
2000US-0608408.
                                                                                 2000US-0234687.
                                                                                                          04-OCT-2000; 2000GB-0024263.
           2001WO-US00669
                                                                       2000US-0632366
                                                                                               2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK11364 standard; DNA; 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.6
Best Local Similarity 61.1
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epilepsy; cancer; ss.
                                                                                                                                                                                 WPI; 2001-483447/52
                                             26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
           30-JAN-2001;
                                                                                 21-SEP-2000;
27-SEP-2000;
                                  04-FEB-2000;
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                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK11364;
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1081 CAGTTATGACATTGGGTTTGGGCTTTATTTGAATGGACAGACTCTCCAAATGCTGCTGT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAAGAGAAAGATTCGGCAGGATGCAGATTCTGTGATTACAGTACGTCGAGGAGAAGTCGT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCGTCCGAGTCCCGACTCATGAGGAAGGATCATACCTATTTTGGGAATTTGCCACAGA 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 AGTCTCCCCACCTCTGATGGCTCCTCCATGCATCTGGACCTTTGCCAAGGTGAAGTT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 TGACTATGACATTGGAGTTTATTTTGGACCTGTAACTAGCACTGTAACTTAGCATTATTTTGGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        901 AGACTCTCTTCCAGTGATTGCAGCTCCATGTGGACAAGACCACAAATCAAAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 CAAAAGCAAGCTGGGCAAAGAGAAGAACAGCCGTCTGGTGGTGAAGCGTGGTGAGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 GACCATCCGGGTACCTACTCATCCAGAGGGAAGCGTGTCTGCTGGGAGTTTGCGACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1141 CAGTGTGCATGTCAGTGAGTCCAGTGACGAGGAGGAGGAGGAGGAGGAAAATG 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO: 11355; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 554 BP; 156 A; 149 C; 114 G; 135 T; 0 other;
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Llarity 61.1%; Pred. No. 1.5e-19;
Conservative 0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                     2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                                               2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK37154 standard; DNA; 554
                                                                                                                          2001WO-US00667
                                                                                                                                                                                        2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                             04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 179; Conserv
WO200157275-A2
                                                                                                                       30-JAN-2001;
                                                                                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                      03-AUG-2000;
                                                                                                                                                                                        04-FEB-2000;
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                                                             09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                961 TAAAGAAGAATTCGGCAGGATGCAGATTCTGTGATTACAGTACGTCGAGGAGAAGTCGT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1021 CACCGTCCGAGTCCCGACTCATGAGGATCATACCTATTTTGGGAATTTGCCACAGA 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1081 CAGTTATGACATTGGGTTTGGGGTTTATTTTGAATGGACAGACTCTCCAAATGCTGCTGT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       901 AGACTCTTCCAGTGATTGCAGCTCCATGTGGACAAGACCACAAATCAAAGACTT 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO: 11711; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%; Score 110.6; DB 22; Length 61.1%; Pred. No. 1.5e-19; ive 0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 554 BP; 156 A; 149 C; 114 G; 135 T; 0 other;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                             analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                     Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                       04-FEB-2000, 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0207408.
03-AUG-2000; 2000US-0232468.
21-SEP-2000; 2000US-0224687.
27-SEP-2000; 2000US-0234687.
                                                                                                              2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 61.1
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                              WPI; 2001-488900/53
                                                    WO200157276-A2
                            Homo sapiens
                                                                                                              30-JAN-2001;
                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                    Penn SG,
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8. g
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Search completed: February 21, 2003, 21:43:11 Job time : 351 secs

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Appli Appl Appl Appl

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Appl Appl Appl Appl

Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3

Sequence Sequence Sequence

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DB 1; Length 7218;
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APPLICATION NUMBER: US/08/232.463
US-09-651-011A-3
US-08-285-440-10
US-08-285-440-11
US-08-285-440-11
US-08-630-349-11
US-08-830-349-13
US-08-830-349-13
US-08-830-349-13
US-08-830-349-13
US-08-9-007-005-32
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US-09-307-005-33
US-09-307-005-33
US-09-307-005-33
US-09-307-005-33
US-09-307-005-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 99.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
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TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
    4266
939
939
11599
11677
11677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-232-463-14/C
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US-08-232-463-14
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COUNTRY:
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    Sequence 20, Appl
Sequence 20, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 15, Appli
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Sequence 209, App
Sequence 93, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                     ; Search time 67 Seconds (without alignments) 6678.230 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                           1 gaattcgcggccgcgtcgac.........catgacgtttaatttccttt 1459
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Patent No. 527
Patent No. 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/AB_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                    version 5.1.3
- 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-298-588-1
US-08-770-379-20
US-08-770-379-20
US-09-230-371A-20
US-09-249-585A-2
US-09-249-585A-2
US-09-359-081-2
US-09-359-081-2
US-08-910-647-1
US-08-910-647-1
US-08-910-647-1
US-08-910-647-1
US-08-911-15
US-08-08-11-15
US-08-08-11-15
US-08-08-11-15
US-08-08-194-0888-15
US-08-194-0888-15
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US-08-781-891-209
US-08-056-200-93
US-08-800-644-93
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                             441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                       February 21, 2003, 21:31:21
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Maximum Match 1008
Listing first 45 summaries
                                                                                                nucleic search, using sw model
                                                                                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                  GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
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1459
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Minimum DB Maximum DB

Database :

Perfect score:

Sequence:

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Run on:

Scoring table:

NAME/KEY:

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                                                                                              GGGGAATGATAGGAGGAGAGAATGGGCAGCTCTGGGAAACATGTCCAAGGAGGATGCCAT 285
                                                                                                                                     GGTAGAGTTTGTGAAGCTTCTAAATAAGTGTTGTCCTCTCCTCTCGGCATATGTTGCGTC 345
                                                                                                                                                                                                          GCGTGAAGAGGAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAAGAGGGAAGCGAGAGGGA
                                                                                                                                                                                                                                                                                                                                              GGAAGACCGGCTGAGACGGGGAGGAGGAAGAGGCGGCGGATAGAGGAAGAGAGCCTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGGAACAGCAAAAGCAGCAGATAATGGCAGCTTTAAAACTCGCAGACTGCC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immediate Early Protein From Kaposi's
Sarcoma-Associated Herpesvirus, DNA
Encoding Same And Uses Thereof
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0575/52268/JPW/MSC/SKS
Pred. No. 5.7e-18;
                Best Local Similarity 2.6%; Pred. No. 5.7e-
Matches 9; Conservative 247; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: More, Patrick S.
TITLE OF INVENTION: Immediate Earl TITLE OF INVENTION: Barcoma-Assor TITLE OF INVENTION: Encoding Same NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08728323A
Patent No. 5948676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) FEATURE:
              2.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-728-323A-1
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CITY: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                 226
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APPLICANT: Rieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Raye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                             1877 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGGATGAGCAGCAGCAGCAGGATGAGCAGC 1936
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Pred. No. 5.6e-11;
0; Mismatches 228;
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                                                     DB 2;
                                                   Score 74.2; DB 2;
Pred. No. 5.6e-11;
0; Mismatches 228
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                                                                     Best Local Similarity 50.3 Matches 236; Conservative
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US-08-728-323A-1
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                                                                                                                                                                                                  CAGCCCAGCAGTAT --- CCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGC
                                                   477 TGAGACGGGAGGAGGAGGAGGCGGCGGATAGAGGAAGAGGCCTTCGGCTGGAACAGC
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STREET: 1185 Avenue of the Americas
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SYSTEM: PC-DOS/MS-DOS
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Patent No. 5849564
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234;
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
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US-08-770-379-20
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LENGTH: 32207 base pairs
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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APPLICANT: Chang,
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STATE: New York
COUNTRY: U.S.A.
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                                                                            537 AAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTATG 596
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Length 32207;
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Score 74.2; DB 2;
Pred. No. 1.9e-10;
); Mismatches 228;
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669
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STREET: 1185 Avenue of the Ame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
5.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : (212) 278-0400
(212) 391-0525
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                                       Conservative
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TITLE OF INVENTION: SE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STATE: New York
                    Similarity
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US-08-757-669A-20/C
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Mismatches 228;

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Matches 236;
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APPLICANT: Bohearzy, Roy A
APPLICANT: Bohearzy, Roy A
APPLICANT: Russo, James J
APPLICANT: Belman, Isidore S
APPLICANT: Belman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNEST THEREOF
FILE REPERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
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                                                                                                                                                                                 0; Mismatches 228; Indels
                                                                                                                                               Ouery Match 5.1%; Score 74.2; DB 4; Best Local Similarity 50.3%; Pred. No. 1.9e-10; Matches 236; Conservative 0; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA; TYPE: DNA; CREANISM: Kaposi's sarcoma-associated herpesvirus US-09-230-371A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/09230371A Patent No. 6348586 GENERAL INFORMATION:
APPLICANT: Chang, Yuan APPLICANT: Bohenzky, Roy A APPLICANT: Russo, James J
                                                                                              MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERLSTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity

Query Match

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                                           20120 AGCAGGATGAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 20061
                                                                                                                       AAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTATG 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            654 AGGAGCAGCACTATCAGCAGTATAAACACCAG--GCAGAGCAAACCCAACCTGCACAACA 711
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APPLICANT: HOTIOK, ROBERT
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REPERENCE: 0867/00905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILIMO DAPE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PAtentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAACGAGAGCGGCTGCAAAAGGAAGAAGAAGAAGCGGAAGCGAGAGGAGGAAGACCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | || ACCAGGAGTTAGAGGAGCAGGAGTTAGAGGATCAGGAGCAGCAGA 19652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           772 ATCAAAGGTGAACACAGCTGGAGCAAGTGATACACTGTCAGTTAATGGA
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LOCATION: (1)..(1926)
OTHER INFORMATION: coding strand of EBNA-1 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Epstein Barr Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 195; Conservative
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LENGTH: 1926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IITLE OF INVENTION: Mammalian Protein Interaction Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2580;
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LIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-Jul-1999
CLASSIFCATION: CURNOWN>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-359-081-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/050,863
FILING DATE: CUNKNOWN>ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09359081
Patent No. 631623
GENERAL INFORMATION:
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STRANDEDNESS: unknown
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Payan, Don
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Patent No. 6114111
GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE: 30-MAR-1998
                                                                                                                                                                                                                                                              GAGGGCAGGAGGGCAGGAGCAGGAGGGG 907
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: S11va, Robin M.
REGISTRATION UNMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Matches 195; Conservative
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COMPUTER READABLE FORM:
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US-09-050-863-2
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STREET: 4
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US-09-050-863-2
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STATE:
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                                        GAAGAACGAGAGGGGCTGCAAAAGGAAGAAGAAGCGGAAGCGAGAGGAGGAAGACCGG
                                                                                                                   CTGAGACGGGAGGAAGAGAGGCGGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09130114
Patent No. 5976807
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Evaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/109030131
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEO ID NOS: 36
SOFTWARE: PastSEO for Windows Version 3.0
SEO ID NO 1.
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48.9%; Pred. No. 2e-10;
Live 0; Mismatches 204; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1252 GAGGGCCAGGAGGGCCAGGAGCAGGGCCAGGAGGGG 1290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                   TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Polynucleotide Delivery
                                                                                 1553 GAGGGCAGGAGGGCCAGGAGCAGGGGCCAGGAGGGG 1515
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                                                 716 GCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/910,647
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                  Sequence 1, Application US/08910647
Patent No. 6251433
GENERAL INFORMATION:
APPLICANT: ZUCKETMANN et al.
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REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                   STRANDOM STREET STREET CITY: EMERYVILLE STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (510) 655-3542 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9600 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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Matches 195; Conserv
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US-08-910-647-1
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NUCLEIC ACID
EDNESS: single
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TOPOLOGY:
US-07-884-811-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAGAGCGGAAGCGAGAGGAGGAGGACCGG 475
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Pred. No. 2.8e-10;
0; Mismatches 204; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                               1298 GAGGGCAGGGCAGGAGGAGGGGCAGGAGGGG 1336
                                                           716 GCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGG 754
                                                                                                                                                                                                                                     TITLE OF INVENTION: Compositions and Method Polynucleotide Delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/620,925
FILING DATE: 21-Uu1-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEPHONE: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-620-925-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/910,647 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
                                                                                                                                                                                                                                                                                                                 STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                      Sequence 1, Application US/09620925 Patent No. 6468986 GENERAL INFORMATION:
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STRANDEDNESS: single
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ZIP: 94608-2916
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                 CITY: Emeryville
STATE: California
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Best Local Similarity 48.9
Matches 195; Conservative
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                         US-09-620-925-1
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                                                                                                                                          RESULT 12
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
                                                                           GAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAACAG
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                                                                                                                                                                            Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                      716 GCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: 5.25 inch, 360 Kb floppy disk IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 3e-10;
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48.9%; Pred. No. 3e
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FILING DATE: 19920518
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                                                                                                                                                                                                                                                                                      Sequence 15, Application US/07884811 Patent No. 5316921 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 3:
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596 GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAG 655
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                                                     536 CAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTAT 595
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OPERAING SYSTEM: PC-LUC,...
OPERAING WinPain (Genentech)
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TELEPHONE: 415/225-5416
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INFORMATION FOR SEQ ID NO: 15:
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REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
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US-08-087-783A-15
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Best Local Simi
Matches 195;
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                536 CAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTAT 595
                                                                                                                                          656 GAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAACAG 715
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                                                                    596 GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAG
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                                                                                                                                                                                                              716 GCAGCATTACAGAAACAGCAAGAAGTAGTGGTGGCTGGG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/07/885,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/07885971
Patent No. 5328837
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin (Genetich)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/86
FILING DATE: 19920518
CLASSIFICATION: 530
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TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
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NAME: Dreger, Ginger R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dreger, Ginger R REGISTRATION NUMBER: 3:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10596 bases
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US-07-885-971-15
                                                                                                                                                                                                                                                                                                                   US-07-885-971-15
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Patent No. 5547856
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R., TITLE OF INVENTION:
TITLE OF INVENTION:
HEPATOCYTE GROWTH FACTOR VARIANTS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                          2832 GAGGGGCAGGAGGGCAGGAGCAGGGGGCAGGAGGGG 2870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72.6; DB 1;
Pred. No. 3e-10;
); Mismatches 204;
716 GCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/087,783A
FILING DATE: 13-Jul-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-92
ATTORNEY/AGERT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P0755779P1
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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416 GAAGAACGAGAGGGCTGCAAAAGGAAGAAGCGGAAGCGAAGGAGGAAGACCGG 475
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| 169 | 35 | 551 |
|---|---|--|
| Db 2532 CAGGAGGGCAGGAGGGCAGGAGCAGGAGGGCCAGGAGGGCAGGGGGG | 476 CTGAGACGGGAGGAGGAGGCGGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAG 535 | Db 2592 CAGGAGGGCAGGAGGAGGGCCAGGAGCAGGAGGAGGAGGA |
| 2532 | 476 | 2592 |
| Op | Οy | QD |

⁵³⁶ CAAAAAGCAGCAGATAAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTAT 595

Db ò

δý Db ò

Search completed: February 21, 2003, 21:47:36 Job time: 271 secs

⁵⁹⁶ GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAG 655

⁶⁵⁶ GAGCAGCACTATCAGCAGTATAAACACCCAGGCAGAGCAAACCCCAACCTGCACAACAACAAGA 715

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RESULT 1
                                                                                                                                                            February 21, 2003, 21:37:16 ; Search time 93 Seconds (without alignments) 8811.096 Million cell updates/sec
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1459
1 gaattcgcggccgcgtcgac......catgacgtttaatttccttt 1459
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/ cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442118 seqs, 280819700 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM nucleic - nucleic search, using sw model
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length: 200000000
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Perfect score:
Sequence:
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | ď | | | CONTRACTES | |
|--------|-------|-------|-----------------|----|---------------------|-------------------|
| Result | | Query | | | | |
| No. | Score | Match | Match Length DB | DB | QI | Description |
| 1 | 204.4 | 14.0 | 934 | 10 | US-09-866-562-33 | Sequence 33, Appl |
| 7 | 113.4 | 7.8 | 527 | 10 | US-09-866-562-32 | Sequence 32, Appl |
| m | 110.6 | 7.6 | 554 | 10 | US-09-864-761-13381 | Sequence 13381, A |
| 4 | 109.2 | 7.5 | 306 | 10 | US-09-864-761-30285 | Sequence 30285, A |
| Ŋ | 69.4 | 4.8 | 720 | 6 | US-10-101-487-74 | Sequence 74, Appl |
| 9 | 69.4 | 4.8 | 720 | 6 | US-10-101-487-76 | Sequence 76, Appl |
| 7 | 8.99 | 4.6 | 575 | 10 | US-09-864-761-20733 | Sequence 20733, A |
| 80 | 9.99 | 4.6 | 1969 | 10 | US-09-864-761-3972 | Sequence 3972, Ap |
| 6 | 65 | 4.5 | 659158 | 6 | US-09-771-208-20 | Seguence 20, Appl |
| 10 | 63.4 | 4.3 | 3809 | 12 | US-10-001-870-68 | Sequence 68, Appl |
| 11 | 62.8 | 4.3 | 2108 | 10 | US-09-962-832-225 | Sequence 225, App |
| 12 | 62.4 | 4.3 | 474 | 10 | US-09-864-761-11284 | Sequence 11284, A |
| 13 | 62 | 4.2 | 522 | σ | US-10-101-487-71 | Sequence 71, Appl |
| 14 | 62 | 4.2 | 530 | 6 | US-10-101-487-73 | Sequence 73, Appl |
| 15 | 62 | 4.2 | 554 | σ | US-10-101-487-69 | Sequence 69, Appl |
| 16 | 62 | 4.2 | 554 | σ | US-10-101-487-106 | Sequence 106, App |
| 11 | 61.8 | 4.2 | 475 | 10 | US-09-864-761-1361 | Sequence 1361, Ap |
| 18 | 61.8 | 4.2 | 512 | 10 | US-09-864-761-18121 | Sequence 18121, A |
| 19 | 61 | 4.2 | 475 | 10 | US-09-864-761-6203 | Segmence 6203. Ap |

| Sequence 22817, A Sequence 27984, A Sequence 2583, Appl Sequence 19707, Appl Sequence 19707, Appl Sequence 931, Appl Sequence 1784, Appl Sequence 18143, Appl Sequence 32, Appl Sequence 34, Appl Sequence 36, Appl Sequence 31, Appl Sequence 35, Appl Sequence 35, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 31, Appl Sequence 31, Appl Sequence 38, Appl Sequence 81553, Appl Sequence 81553, Appl Sequence 81553, Appl Sequence 81551, Appl | App. |
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| US-09-864-761-22817 US-09-864-761-27984 US-10-001-873-22 US-09-2864-761-27984 US-09-864-761-19707 US-09-864-761-2926 US-09-864-761-2926 US-09-764-853-937 US-09-764-853-933 US-09-764-853-933 US-09-764-853-933 US-09-864-761-19674 US-09-864-761-19674 US-09-864-761-19674 US-09-864-761-19674 US-09-864-761-19674 US-09-864-761-19674 US-09-864-761-19674 US-09-880-1107-2406 US-09-9818-264-3 US-09-9818-264-3 US-09-9818-264-3 US-09-864-761-21553 US-09-864-761-21553 US-09-864-761-1815 | US-09-822-846-491 US-10-095-407-16 US-09-880-107-3945 US-09-864-761-18684 |
| 110000000000000000000000000000000000000 | 9 10 10 |
| 511 267 287 22387 22387 22387 2656 4056 4054 4547 4547 53226 53226 3613 3613 | 2614 152331 20556 272 |
| 44444444444466666666666666666666666666 | 33.7 7.0 8.7.7 7.0 |
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| 0 1 3 3 3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 | 444 444 5445 |
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ALIGNMENTS

| 0S-09 | US-09-866-562-33 |
|----------|---|
| ; Seq.; | Sequence 33, Application US/09866562 Patent No. US20020009758Al |
| ; GEN | |
| A A P | APPLICANT: Harlocker, Susan L. APPLICANT: Wang. Tongtong |
| ; AP | |
| ; AP | |
| ; API | APPLICANT: Switzer, Anne |
| H | TILLE OF INVENTION: COMPOSITIONS AND METRODS FOR THE INERARI TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER. |
| ; FI | FILE REFERENCE: 210121.502 |
| CO | CURRENT APPLICATION NUMBER: US/09/866,562 |
| | CURRENI FILING DAIE: ZULT US ZS NUMBER OF SEO ID NOS: 96 |
| ; SEQ | SEQ ID NO 33 |
| Ξi | LENGTH: 934 |
| | TYPE: DNA ORGANISM: Homo sapiens |
| 0S-09 | US-09-866-562-33 |
| One | Query Match 14.0%; Score 204.4; DB 10; Length 934; |
| Mate | vative 2 |
| οy | 1158 AGTCCAGTGACGAGGAGGAGGAAGGAAAATGTCACTTGTGAAGAAAAAA 1217 |
| Dp | 3 AGGCCAGCGATGACGACGAGGAGGAAGAAGGAAACATCGGTTGTGAGAGAGA |
| Oy | 1218 AGAACGCCAACAAGCCTCTGCTGGATGAGATTGTACCTGTGTACCGGGGGGACTGTCACG 1277 |
| QQ | 63 AGAATGCCAACAAGCCTTTGCTGGATGAGATTGTGCCTGTGT-CCGACGGACTGTGTG 121 |
| Qγ | 1278 AGGAAGTATATGCAGGCAGCCACCAGTATCC-AGGGAGGGGAG |
| Dp | 122 AGGATGTGTATGCTGGGAGCCATCAATATCCAAGGGAGAGGAGTCTATCTCCTCAAGTT 181 |
| οy | 1337 GATAATTCCTACTCTGTGGAGGTCCAAGTCCGTCTACTACAGAGTCTATATATA |
| ī | |
| DP DP | 182 GACAACTCCTACTCTTTGTGGCGGTCAAAATCAGTCTACTACRGAGTCTATTATACTAGA 241 |

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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 13381
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Sequence 13381, Application US/09864761

Sequence 13381, Application US/09864761

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Tank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-04

PRIOR FILING DATE: 2000-09-04

PRIOR FILING DATE: 2000-09-04

PRIOR FILING DATE: 2000-09-04

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2000-09-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1365 AGTCCGTCTACTACAGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTC 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
1397 TAGAGCTGCTGTTCCAAGGTCCGGAGTCCAGGGTTGAGCACAACATGACGTTTAATTT 1454
                            Sequence 32, Application US/09866562
Fatent No. US20020009758a1
GENERAL INFORMATION:
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: ADD DIAGNOSIS OF LUNG CANCER.
FILE REFERENCE: 210121.502
CURRENT APPLICATION UNMBER: US/09/866,562
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 32
LENGTH: 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TAGGGTTGGCCAGAAGATGACATTTAATTT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(527)
; OTHER INFORMATION: n = A,T,C or G
US-09-866-562-32
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Best Local Similarity 84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
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                                                                                                              RESULT 2
US-09-866-562-32
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1081 CAGTTATGACATTGGGTTTGGGGTTTATTTTGAATGGACAGACTCTCCAAATGCTGCTGT 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1021 CACCGTCCGAGTCCCGACTCATGAGGAAGGATCATACCTATTTTGGGAATTTGCCACAGA 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 CAAAAGCAAGCTGGGCAAAGAAAGAAAGAGCCGTCTGGTGGTGGAGCGTGGTGAGGTGGTG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 GACCATCCGGGTACCTACTCATCCAGGGGAAGCGTGTCTGCTGGGGGTTTTGCGACCGA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901 AGACTCTTCCAGTGATTGCAGCTCCATCCATGTGGACAGAGACCAAAATCAAAGACTT 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 AACTGTGCAGGTCAGTGGATTCCAGTGACGATGAGGAAGAGGAAGAGG 191
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N: EXPRESSED IN BRAIN, SIGNAL = 1.9

N: EXPRESSED IN PLACENTA, SIGNAL = 1.8

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

N: EXPRESSED IN LUVER, SIGNAL = 1.6

N: EXPRESSED IN LUVER, SIGNAL = 1.7

N: EXPRESSED IN HELA, SIGNAL = 1.7

N: EXPRESSED IN HELA, SIGNAL = 1.7
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR PILING DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLILOGATION NUMBER: PCT/USO1/00669
PRIOR PLILOGATION NUMBER: PCT/USO1/00665
PRIOR PELING DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PLILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PLILNG DATE: 2000-09-21
PRIOR PLILNG DATE: 2000-09-21
PRIOR PLILNG DATE: 2000-09-30
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; Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 179; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

OTHER INFORMATION: M.
OTHER INFORMATION: E.
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APPLICANT: TOMPKINS, CHISTOPHER K.
APPLICANT: TOMPKINS, CHISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT APPLICATION NUMBER: 60/277,705
PRIOR APPLICATION NUMBER: 60/277,705
NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                   1084 TTATGACATTGGGTTTGGGGTTTATTTTGAATGGACAGACTCTCCAAATGCTGCTGTCAG 1143
                                                                       GGAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAAGAGGGAAGCGAAGCGAGGAGGAAGACG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 GCTGAGACGGGAGGAGGAGAGAGAGGCGGCGATAGAGGAAGAGAGGCCTTCGGCTGGAACA 534
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                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 3e-09;
); Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 74, Application US/10101487 Patent No. US20020169125A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LEUNG, DAVID W.
APPLICANT: BERGMAN, PHILIP A.
APPLICANT: LOFQUIST, ALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.6
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (2)..(718)
US-10-101-487-74
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SEQ ID NO 74
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LOCATION: (2)
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                                                                       1024
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                                                                  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
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N: EXPRESSED IN PLACENTA, SIGNAL = 1.6
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
N: EXPRESSED IN LUNG, SIGNAL = 2.4
N: EXPRESSED IN LUNG, SIGNAL = 2.4
N: EXPRESSED IN HELA, SIGNAL = 1.7
N: M: EXPRESSED IN HELA, SIGNAL = 1.7
N: M: TAFO22770.2, EVALUE 3.00e-03
N: M: SMISSPROT HIT: P49193, EVALUE 1.30e-01
N: EST_HUMAN HIT: AW292776.1, EVALUE 0.00e+00
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Pred. No. 2.1e-20;
0; Mismatches 113;
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-36
PRIOR PELICATION NUMBER: US 09/632, 366
PRIOR PELICATION NUMBER: US 02/26, 359
PRIOR FILING DATE: 2000-09-37
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR FILING DATE: 2001-01-30
                                                                                                               FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER: PCT/US01/00668
2001-01-30
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APPLICATION NUMBER: PCT/US01/00670
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Rank, David R.
Hanzel, David K.
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Matches 177; Conserv
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LENGTH: 306
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655 GGAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAACA 714

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US20020048763A1
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                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LEUGG, DAVID W.
APPLICANT: LEUGG, DAVID W.
APPLICANT: LEUGG, DAVID W.
APPLICANT: LOFQUISY, ALAN
APPLICANT: TOMFKINS, CHRISTOPHER K.
APPLICANT: TOMFKINS, CHRISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 077319/0329
CURRENT FILING DATE: 2002-03-20
FRIOR APPLICATION NUMBER: 60/277,705
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR APPLICATION NUMBER: 60/277,705
SPIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 76
LENGTH: 720
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415 GGAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAAGAGGGAAGCGAAGGGAGGAAGACCG 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             535 GCAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTA 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              655 GGAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAACA 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.8%; Score 69.4; DB 9; Length 720; Best Local Similarity 48.6%; Pred. No. 3e-09; Matches 190; Conservative 0; Mismatches 201; Indels
                                                         715 GGCAGCATTACAGAAACAGCAAGAAGTAGTG 745
                                                                                                679 AGAGGAGGAAGAGGAAGAGAGAGAGAG 709
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                                                                                                                                                                                                 Sequence 76, Application US/10101487 Patent No. US20020169125A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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US-09-864-761-20733
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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR APPLICATION NUMBER: PCT/USO1/00665
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EST_HUMAN HIT: BE071749.1, EVALUE 5.80e+00
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N: EXPRESSED IN ADULT LIVER, SIGNAL = 11
N: EXPRESSED IN BT474, SIGNAL = 11
N: EXPRESSED IN BRAIN, SIGNAL = 14
N: EXPRESSED IN BONE MARROW, SIGNAL = 12
N: EXPRESSED IN PLACENTA, SIGNAL = 12
N: EXPRESSED IN HEART, SIGNAL = 9.4
N: EXPRESSED IN HEART, SIGNAL = 11
N: EXPRESSED IN HEART, SIGNAL = 11
N: EXPRESSED IN HEART, SIGNAL = 11
N: EXPRESSED IN HEART, SIGNAL = 12
N: EXPRESSED IN HEART SIGNAL = 12
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ilarity 49.7%; Pred. No. 1.4e-08;
Conservative 0; Mismatches 197;
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PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-09-21
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
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APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 196; Conserv
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W: EXPRESSED IN HELA, SIGNAL = 13

W: EXPRESSED IN ADULT LIVER, SIGNAL = 11:

W: EXPRESSED IN BT474, SIGNAL = 11

W: EXPRESSED IN BT474, SIGNAL = 11

W: EXPRESSED IN LUNG, SIGNAL = 14

W: EXPRESSED IN BONE MARROW, SIGNAL = 9.4

W: EXPRESSED IN HEART, SIGNAL = 11

W: EXPRESSED IN HEART, SIGNAL = 11

W: EXPRESSED IN FETAL LIVER, SIGNAL = 11
                                                                                                                                                                             Annomax Sequence Listing Engine vers. 1.1
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Pred. No. 2.7e-08;
); Mismatches 197;
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APPLICANT: BRADFORD, ERTC
APPLICANT: BRADFORD, ERTC
APPLICANT: HORVAT: SINON
TITLE OF INVENTION: CLOMING OF A HIGH-GROWTH GENE
FILE REFERENCE: 407T-923710US
CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILING DATE: 2001-01-26
PRIOR PRPLICATION NUMBER: US 08/999,477
PRIOR FILING DATE: 1997-12-29
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PAPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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Patent No. US20020155564A1
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Best Local Simil
Matches 196; C
                                                                                                                                                                             SOFTWARE: Anno
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                                                                                               GAAGAACGAGAGGGCTGCAAAAGGAAGAAGAAGAAGCGGAAGGAGGAGGAAGACCGG
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PRIOR PAPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 09/632,366
PRIOR PELING DATE: 2000-09-03
PRIOR PELING DATE: 2000-00-03
PRIOR PELING DATE: 2000-00-03
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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Patent No. US20020048763A1
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: HARZEL, David K.
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Pred. No. 2.1e-06;
0; Mismatches 80; Indels 0
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LOCATION: (271829)..(271848)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (183872)..(183891)
OTHER INFORMATION: n is unidentified a,
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OTHER INFORMATION: n is unidentified a,
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                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (602466)..(602485)
OTHER INFORMATION: n is unidentified
NAME/KEY: misc_feature
LOCATION: (546998)..(547017)
OTHER INFORMATION: n is unidentified
                                                                                                                                                                                                                                                                                                                     LOCATION: (346860)..(346823)
OTHER INFORMATION: n is unidentified
NAME-KEY: misc_feature
LOCATION: (317174)..(317193)
OTHER INFORMATION: n is unidentified
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LOCATION: (132680)..(132700)
OTHER INFORMATION: n is unidentified
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LOCATION: (494715)..(494814)
OTHER INFORMATION: n is unidentified
NAME/KEY: misc_feature
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LOCATION: (280353)..(280373)
OTHER INFORMATION: n is unidentified
                                                                                                             LOCATION: (123459)..(123478)
OTHER INFORMATION: n is unidentified
                                                                                                                                                                                                                                                                           LOCATION: (39086)..(391005)
OTHER INFORMATION: n is unidentified
NAME/KEY: misc_feature
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; OTHER INFORMATION: n is a, c, g, or
US-09-771-208-20
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             PatentIn version 3.0
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58.5%;
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Best Local Similarity 58.5
Matches 113; Conservative
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                                                                 ORGANISM: Mus musculus
                                                                                              NAME/KEY: misc_feature
NUMBER OF SEQ ID NOS:
                          SEQ ID NO 20
LENGTH: 659158
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US-10-001-870-68
                                                     TYPE: DNA
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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghing
APPLICANT: Liu, Chenghing
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a
FILE REFREENCE: DEX-0283
CURRENT APPLICATION NUMBER: US/10/001,870
CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT APPLICATION NUMBER: US/00/235,077
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR PELING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
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Pred. No. 3.4e-07;
0; Mismatches 91;
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Pred. No. 3.6e-07;
0; Mismatches 202;
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                                                                                                                                                                                                                                                                                                                                                                                                          4.3%;
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Best Local Similarity 47.7
Matches 184; Conservative
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Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapien
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APPLICANT: LEUNG, DAVID W.
APPLICANT: LEUNG, DAVID W.
APPLICANT: LEUNG, DAVID W.
APPLICANT: LEONGUIST, ALAN
APPLICANT: LOFQUIST, ALAN
APPLICANT: TOMPKINS, CHRISTOPHER K.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
FILE REFERENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
PRIOR PILING DATE: 2002-03-20
PRIOR FILING DATE: 2003-03-21
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                                                                                                                                                                 ; OTHER INFORMATION: MAP TO AC003065.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.53
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.66
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.52
US-09-864-761-11284
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                       SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11284
LENGTH: 474
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Pred. No. 2.8e-07;
0; Mismatches 205
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NUMBER OF SEQ ID NOS: 49117
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Matches 185; Conservative
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17; Conservative
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SOFTWARE: PatentIn Ver. 2
                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                            FEATURE:
OTHER INFORMATION: MOTHER INFORMATION: EOTHER INFORMATION:
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; LOCATION: (1)..(522)
US-10-101-487-71
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Best Local S
Matches 117
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1216 TGGTGCAGCAGGAGGGCAGCTGAAGCATCTGGTGCAGCAGGAGGGGCAGCTGGAGCAGC 1275
                                                                                      1396 AGGTGGGGCAGCCAAAGAACCTGGAGCAGGAGAAACAACTGGAGCTCCCAGAGCAGC 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                            1456 AAGAGGCCCAGGTGAAGCACCTGGAGAAGCAGGAGGCACAGCTGGAGCTCCCAGAGCAGC 1515
                                                                                                                                                               AGCAAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGT 593
                                                                                                                                                                                                                                                                          ATGCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGC 653
                                                    474 GCCTGAGACGGAGGAGGAAGAGAGGCGGCGGATAGAGGAAGAGGAGGCTTCGGCTGGAAC 533
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CURRENT FILING DATE: 2001-05-23
PRIOR PPLICATION NUMBER: US 60/180,312
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-06-26
PRIOR PLING DATE: 2000-06-08-38
PRIOR PLING DATE: 2000-09-04
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-13
PRIOR PLING DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
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RESULT 15
US-10-101-487-69
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Sequence 73, Application US/10101487

Patent No. US20020169125A1

GENERAL INFORMATION:

APPLICANT: LEGING, DAVID W.

APPLICANT: PIETZ, GREGONE.

APPLICANT: TOMPKINS, CHRISTOPHER K.

APPLICANT: TOMPKINS, CHRISTOPHER K.

APPLICANT: TOMPKINS, CHRISTOPHER K.

APPLICANT: TOMPKINS, CHRISTOPHER K.

TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 077319/0329

CURRENT APPLICATION NUMBER: 60/277,705

PRIOR APPLICATION NUMBER: 60/277,705

PRIOR FILING DATE: 2001-03-21

SOFTWARE: PATENTIN VOR: 2.1

SOFTWARE: PATENTIN VOR: 2.1
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 596 GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAG 655
                                                                                                                                                                                                                    GAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAACAG 715
                                                                                                                                                                                                                                                              416 GAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAAGCGGAAGCGAAGAGGGAAGACCGG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAGACGGGAGGAGGAGAGAGGCGGCGGATAGAGGAAGAGGCCTTCGGCTGGAACAG 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        536 CAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTAT 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                             476 CTCAGACGGAGGAGGAGGAGAGGCGGCGGATAGAGGAAGAGGCTTCGGCTGGAACAG
                          GAAGAACGAGAGCGCCTGCAAAAGGAACAAGAAGAAGCGGAAGCGAAGAGGAAGACCGG
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Pred. No. 2.8e-07;
0; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                   GCAGCATTACAGAAACAGCAAGAAGTAGTG 745
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Best Local Similarity 47.4%;
Matches 185; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION:
) OTHER INFORMATION:
US-10-101-487-73
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APPLICANT: PIETZ, GREGOY E.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: WGGONER JR., DAVID W.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES TITLE OF INVENTION: THEREOF FILE REPRENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR PILING DATE: 2001-03-21
NUMBER OF SEC ID NOS: 116
SOFTWARE: Patentin Ver. 2.1
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GAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAGAAGCGGAAGCGAGGAGGAGGAAGCGG 475
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                                                                          GCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCTCATCCGCCAGCTGCAG
                                                                                                                                                                            GAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCAACCTGCACAACAACAG
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Pred. No. 2.9e-07;
0; Mismatches 215;
                                                                                                                                                                                                                                                                                 GCAGCATTACAGAACAGCAAGAAGTAGTG 745
                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 69, Application US/10101487 Patent No. US20020169125A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.0%;
Matches 191; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FALGIL NO. CLASSION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEUNG, DAVID W.
APPLICANT: BERGMAN, PHILIP A.
APPLICANT: LOFQUIST, ALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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; LOCATION: (1)..(528)
US-10-101-487-69
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Search completed: February 21, 2003, 23:59:11 Job time : 1928 secs

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| 33.3 493 10 BB704602 31.0 600 13 B1990454 31.0 625 10 AW963720 29.6 984 12 BE916087 29.6 984 12 BE916087 25.8 1194 12 BE694778 25.3 1114 BM64990 25.1 489 10 AW631077 24.0 449 12 BE53826 24.0 461 13 B133401 23.7 77 49 BE52428 23.7 77 40 BE541801 22.5 77 41 BB6180483 23.3 592 14 BM61531 22.5 77 4 10 BE541801 22.4 895 14 BM601531 22.5 77 4 10 BE741801 22.6 462 14 N31282 20.7 476 10 BE748877 21.1 434 9 AL60409 20.6 462 14 N31282 20.7 475 10 BE768885 21.1 434 9 AL67403 20.1 614 9 AL67543 | 28.6 19.1 421 9 A656630 278.6 19.1 431 12 BG080930 277 19.0 828 13 B1868335 273.2 18.7 450 9 A1506318 273.2 18.7 450 9 A1506318 271.6 18.6 496 1388 9 A148726 271.4 18.3 390 14 C87779 267.4 18.3 407 14 C85460 267.4 18.3 411 14 C85479 267.4 18.3 411 12 BG067872 | BG294067 757 bp mRNA lin ION 60239930F1 NIH_MGC_94 Mus musculus cDNA clone mRNA sequence. N BG294067 1 G1:13054331 S EST. NOUSE mouse. ISM Mus musculus Eukaryota: Metazoa; Chordata; Craniata; Verteb Mammalia; Eutheria; Rodentia; Sciurognathi; Mu C bases 1 to 757) RS NIH-MGC http://mgc.nci.nih.gov/. | TITLE NATIONAL INSTITUTES OF Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) CONTACT: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10372 row: k column: 08 High quality sequence stop: 680. FEATURES 1. 757 |
|---|--|--|---|
| · · · · · · · · · · · · · · · · · · · | | REES BG22 BG22 BG22 BG23 BG23 BG23 BG33 BG33 | COO, J. |
| GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: February 21, 2003, 21:36:46; Search time 2217 Seconds (without alignments) 10658.194 Million cell updates/sec Title: US-09-762-594-2 Sequence: 1459 Sequence: 1459 Scoring table: IDENTITY_NUC Gaper 1.0 Searched: 16154066 seqs, 8097743376 residues Total number of hits satisfying chosen parameters: 32308132 Minimum DB seq length: 200000000 Maximum Match 100% Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries | ST:* em_esthum: em_estin:* gb_esti:* gb_esti:* gb_esti:* | | grea grea s der 5.6 5.6 7.4 |

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932 bp mRNA linear EST 02-MAY-2002
AGENCOURT_7551342 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6066023
5', mRNA sequence.
                                                                                                                                                                                                                                       .
9
                                                       /tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full:length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                          DB 12; Length 757;
                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                        40.9%; Score 597.4; DB 12; 96.6%; Pred. No. 5.9e-131; iive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGAGTCTAGGGTTTGAGCACAACATGACGTTTAATTTCCTTT
/organism="Mus musculus"
                                           /clone_lib="NIH_MGC_94"
            /db_xref="taxon:10090"
/clone="IMAGE:4502911"
                                                                                                                                                                                                                                     679; Conservative
                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                           Local
                                                                                                                                                              BASE COUNT
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DEFINITION

ACCESSION

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:960603"
/clone=llb="NIH_MGC_72"
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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT
                                                                     Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 932)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCATAAGCAAGTTCTTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATGCCATGGTAGAGTTTGTGAAGCTTCTAAATAAGTGTTGTCCTCTCCTCTCGGCATA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGAAGGCAGCGTGAAGAGGAACGAGAGCGGCTGCAAAAGGAAGAAGAGAAGAGGAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGAGAGGAGGAAGACCGGCTGAGACGGGAGGAGGAAGAAGAGGCGGCGGATAGAGGAAGA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Argayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM13343 row: d column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGAGAAGAAGAAAGGCTTCGACGGGAGGAAGAGAAAAGGAGACGGATAGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGCTTCGGCTGGAACAGCAAAAGCAGCAGATAATGGCAGCTTTAAAACTCGCAGACTGC
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                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 555.6; DB 14; Length 932;
Pred. No. 4.7e-121;
0; Mismatches 134; Indels 5;
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                                                                                                                                                                                                                                                                                                                                   High quality sequence start: 20
High quality sequence stop: 395.
Location/Qualifiers
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   GI:20404572
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197 c
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llarity 82.8%;
Conservative (
                                                   Homo sapiens
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/db_xref="taxon:9606"
/db_xref="csblo29y106"
/clone="csblo29y106"
/clone="lbplacenta"
/tissue_type="placenta"
/rissue_type="placenta"
/rote="wector: pCWWSPORT 6; Site_1: NotI; ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockwille, maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL: http://fullength.invitrogen.com"
8 a 221 c 305 g 159 t 2 others
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Tai,W.B., Gruber,C., Jessee,J. and normalization
Unpublished (2001)
Contact: Genoscope
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BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                 CGTGCAATTCCAGCAGTATGCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGAT
                TCTCATCCGCCAGCTGCAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAAC
                                                                                                      CCAACCTGCACAACAACAGGCAGCATTACAGAAACAGCAAGAAGTAGTGGTGGCTGGGGC
                                                                                                                                 CCAGCTTTCACGGCAACAGGCAGCATTACCGAAACAACCGGAAGTAGTAGTGGCTGGGTC
                                                                                                                                                                       ATCATTGCCTGCATCATCAAAGGTGAACACAGCTGG-AGCAAGTGATACACTGTCAG-TT
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Pred. No. 6.4e-118;
1; Mismatches 88;
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BG254119 1108 bp mRNA linear EST 13-FEB-2001 602367007F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4475329 5',
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1 (bases 1 to 1108)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10300 row. n column: 02
High quality sequence stop: 640.
Location/Qualifiers
TGATGTGTTGGGGAATGATAGGAGGAGAATGGGCAGCTCTGGGAAACATGTCCAAGGA
                                                                                                                                                                                                   GCGAAGGCGNCGTGAAGAAGAAGAAGAACGTCTGCAAAAGGAGGAAGAAAGGTAG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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BASE COUNT

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/Lissue_trype="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Sfil (ggccgctcggcc); Site_3: Sfil (ggccattatggcc);
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Catarrhini; Hominidae, Homo.
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NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can tfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCMI662 row; g column: 16
High quality sequence stop: 704.
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIH_MGC_59"
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Mammalia; Eutheria; Primates;
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                                                                                                                                                  /tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)." |
/lab_host="DH10B (phage-resistant)." |
/lote="Organ: prostate; Vector: pCWW-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4475329"
                                                                                                                     /clone_lib="NIH_MGC_91"
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                                                                                                                                                                                                                                                                                                                                               BG705952 707-bp mRNA linear EST 07-MAY-2001 602669271F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4792145 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 707)
1318
                                                                                                                       GTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTGGAGGTCCAAGTCCGTCTACTAC 1378
                                                                                                                                                                                1379 AGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTCCAGGGTTGAGCACA 1438
                                                                        NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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http://image.lhnl.gov
Plate: LLAM10669 row: n column: 18
High quality sequence stop: 706.
Location/Qualifiers
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Pred. No. 6e-105;
); Mismatches 79;
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/db_xref="taxon:9606"
/clone="IMAGE:4792145"
/tlssuc_type="hypthalamus"
/lab_host="DH108"
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87.3%;
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                                                                                                                                                                                                                                                          Query Match 33.4
Best Local Similarity 87.3
Matches 557; Conservative
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BG705952
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BB704602 BIREN full-length enriched, in vitro fertilized eggs Musmusculus CDNA clone 7420455P14 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1358 AGGTCCAAGTCCGTCTACTACAGAGTCTATTATACTAGAT-AGAGCTGCTGTTCCAAGGT 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCAGTATCCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTGG 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATITITGGGAATITGCCACAGACAGTTATGACATIGGGTTTGGGGTTTATTTGAATGG 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGTGGGCCGAGGAGAAGTGGTCACTTCGAGTACCCACCATGAAGAAGGATCATAT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGAAGAAGAAGAACATC-GTTGTGAAGAGAAAGCCAAAAAGAATGCCAAACAAGCCTTTG 422
GAAGCCTTGGAAAATGGACCAAAAGACTCTTCCAGTGATTGCAGCTCCATCTGG
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Contact: Yoshihide Hayashizaki
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Contact: Klein WH
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                                                                                                                                                                                                                                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAGAGAGGAGCACTCTTTTTTTTTTTTTTTTVN 3'), cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI" 102 c 125 g 107 t
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                                                     Email: genome-resegsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected CDNAs to
                                                                                                                                                  prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was primed with a primer [5'
  Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCCACACTGAAAATTCCGAAAAAGTCCTTGAGCCAGAAGCTGCAGAAGAAGCTTGGA 888
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/clone_lib="RIKEN full-length enriched, in vitro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="in vitro fertilized eggs"
/dev_stage="egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.3%; Score 485.6; DB 10
99.2%; Pred. No. 1.8e-104;
iive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="female
1-7.-22 Suehiro-cho, T
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc
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/dev_stage="embryonic day 14.5 post-fertilization"
//note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dT. MRA Isolation: cytoplasmic RNA preps
(Manniatis); Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TACGTCCATGATTCTGAGTC.
Information regarding entire library may be found at
they://pa.swmed.edu/Data/Libraries/microarray_cdna_librar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B1990454 600 bp mRNA linear EST 20-DEC-2001 4071-42 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA, mRNA sequence.
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Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W., White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H. Gene expression in the developing mouse retina by EST sequencing and microarray analysis.
                                                                                                                                                                                                                                                                                                                                       1.188
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/clone_lib="Mouse E14.5 retina lambda 2AP II Library"
/tissue_type="neural retina"
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                                                                                                         1069 ATTTGCCACAGACAGTTATGACATTGGGTTTTGGGGTTTTTGAATGGACAGACTCTCC
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Pred. No. 1.3e-96;
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Eukaryota; Metacoa; Chordata; Catarrhini; Hominidae; Homo.

L (bases 1 to 625)

S Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt, J., Saed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.

Assessment of gene expression patterns in a model of colon tumor metactasis using a 19,200 element cDNA microarray

L Unpublished (2000)

Contact: John Quackenbush

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528
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and
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                       216
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                                                                            627 AACAGCAGATTCTCATCCGCCAGCTGCAGGAGCAGCACTATCAGCAGTATAAACACCAGG 686
                                           254
                                                                                                             GGATGCCATGGTAGAGTTTGTGAAGCTTCTAAATAAGTGTTGTCCTCCTCCTCTCGGCATA 336
                                                                                                                                                                                                     GCGAAGGCAGCGTGAAGAAGGAAGAACGAGAGCGGCTGCAAAAGGAAAGAAGAAAGGAA 456
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AATAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAAACTGAAGTTCGTGGCACT 194
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/clone_lib="MAGE resequences, l
/note="Vector: pBluescript5Km"
134 c 155 g 129 t
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84.8%;
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Plate: 192
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Best Local Similarity 84.8
Matches 530; Conservative
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BE916087 649 bp mRNA linear EST 29-SEP-2000 601666710F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3966651 5',
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMB140 row: c column: 04
High quality sequence start: 8
High quality sequence stop: 640.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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BE916087
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/organism="Mus musculus"

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Query Match
                                                                                                                                                                                         source
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                  REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                 12;
                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                       TGGCAGCTTTAAACTCGCAGA--CTGCCGTGCAATTCCAGC-AGTATGCAGCCCAGC-AG 607
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                                                                                                                                              Length 649;
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                                                                                                                                                                 Indels
                 /clone="IMAGE:3966651"
/clone_lib="NCI_CGAP_Man1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
                                                                                                                                             tch 30.5%; Score 445.4; DB 12; al Similarity 92.5%; Pred. No. 6e-95; 602; Conservative 0; Mismatches 31;
         /db_xref="taxon:10090"
/strain="FVB/N"
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BF797451.1 GI:
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Homo sapiens

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Euteleostomi;
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/lab_host="DH10B (phage-resistant)"
/note="Goran: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full:length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arraped by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9952 row: f column: 04
High quality sequence stop: 702.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 984)
                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Pred. No. 1.3e-91;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NIH_MGC_85"
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/clone="IMAGE:4340355"
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illarity 87.8%;
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(Acganism="Homo sapiens"

(Ab_xref="taxon:9606"

(Aclone_lib="BT0759"

(Aev_stage="Adult"

/note="Corgan: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196

from ORESTES PCR (U.S. Letters Patent application No. 196

into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases I to 519)

1 bass Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts//gethtml2.pl?tl=&t2=PMl-BT0759-200 Seq primer: puc 18 forward High quality sequence start: 22 High quality sequence start: 22 High quality sequence stort: 519.
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                                                                                                                                 BE694778 519 bp mRNA linear EST 11-SEP-200
PMI-BT0759-200700-006-c03 BT0759 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 2.2e-85;
0; Mismatches 60;
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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BE694778.1 GI:10081938
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88.0%;
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/db_xref="taxon:10090"
/clone="InAGE:5706182"
/clone="lib="NIH_BMAP_EXO"
/tissue_type="whole brain"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/tab_host="mlu0B (TI phage resistant)"
/tab_host="Drain: Vector: pYX-Asc; Site_1: EcoR I;
/toe_1: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BO180694 682 bp mRNA linear EST 30-APR-2002 UI-M-EXO-bxc-c-15-0-UI.rl NIH_BMAP_EXO Mus musculus cDNA clone IMAGE:5706182 5', mRNA sequence.
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INTH-MGC http://mgc.nci.nih.gov/.
NITH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov acontact: Nobert Strausberg, Ph.D. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
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This clone was contributed by the Brain Molecular Anatomy Project
TATGACATTGGGTTTTGGGTTTTTTTGAATGGACAGACTCTCCAAATGCTGTGTCAGT 1144
                                                                                                                                                                                                                                                                                                  1145 GTGCATGTCAGTGAGTCCAGTGACGAGGAGGAGGAGGAAGAAAAATGTCACTTGTGAA 1204
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                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Dr.M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be
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                                                                          GTTCGAGTACCCACCATGAAGAAGGATCATATCTTTTTGGGAATTTGCCACAGACAAT 258
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                                                                             University of lowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutues of Mental Health (INIMI), Hemin Chin, Ph.D., program coordinator."
                ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pix-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GTGCGTGGAA. This library was created for the
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AGENCOURT_6490228 NIH_MGC_125 Homo sapiens CDNA clone IMAGE:5725757
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NIH-WGC http://mgc.nci.nih.gov/.
cDNA was size selected according to mRNA size fraction,
                                                                                                                                                                                                                                                                                              290 AATAAAAGGTAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 349
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                               GCATAAGCAAGTTCTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT
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                                                                                                                                                                                                       Score 390.4; DB 14; Length 682; Pred. No. 6.4e-82; 0; Mismatches 2; Indels 0;
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Plate: LLAM12717 row: c column: 06
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
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Location/Qualifiers
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Best Local Similarity 99.5%;
Matches 391; Conservative
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//note="Organ: liver; Vector: PONR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
sequence: S'-CACGGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTACAGGCCGAGGCGCCACATG-CT(30)BN-3' (where B = A,
c, of and N = A, c, G, or T). Average insert size 1:85
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NHL MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                      NIH MGC http://mgc.nci.nih.gov/.

NIH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llni.gov

Plate: LLCM1533 row: h column: 01

High quality sequence stop: 627.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 639)
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                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo saplens"
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/clone="IMAGE:4700208"
/clone=lib="NIH_MGC_76"
/lab_host="DH10B (TI phage-resistant)"
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ATCAAAGACTT-TAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGATTAC ÓΣ g

Search completed: February 21, 2003, 23:27:09 Job time: 2239 secs

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GenCore version 5.1.3
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| OM nucleic - nucleic search, using sw model | February 21, 2003, 21:31:46; Search time 3906 Seconds (without alignments) 10870.710 Million cell updates/sec | |
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| - nucleic search, | February 21, | |
| OM nucleic | Run on: | |

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|---------------------------------------|--|
| Title: Perfect score: Sequence: | US-09-762-594-2 1459 1 gaattcgcggccgcgtcgaccatgacgtttaatttccttt 1459 |
| Scoring table: | IDENTITY_NUC Gapop 10.0 , Gapext 1.0 |
| Searched: | 2054640 segs, 14551402878 residues |
| Total number of | Total number of hits satisfying chosen parameters: 4109280 |
| Minimum DB seq] | Minimum DB seq length: 0 Maximum DB seq length: 2000000000 |

| *0 | 100% | 45 summaries | |
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| H 2 E 4 | 1 1 | Match | Length | | ID | | 101341111111 | |
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| w 4 | 1340.6 | 91. | 543 140 | 10 | AF02277 AK025520 | | AF022770 AK025520 | Mus |
| 7" | 1079.6 | 74. | 3598 | | AB043587 | | AB043587 | Homo sapi |
| S | 287.2 | 19. | 18140 | C | AF501319 | | AF501319 | Mus muscu |
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| | 238 | 16. | 140409 | | AC044825 AL592045 | | ACU44825 AL592045 | HOMO Sapi Homo sapi |
| 6 0 | 238 | 16. | 232180 | | AC021883 | | AC021883 | Homo sapi |
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| 7 | 95 | 9. | 264522 | | AC090437 | | AC090437 | Mus muscu |
| 7 0 | ~ ر | | 184865 | | AC11081/ AL807824 | | AC11081/ AL807824 | Mus muscu |
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| m r | . ი | | 190594 | 0 | AL606965 | | AL606965 | Mouse DNA |
| 37 0 | | | 225045 | | ACU96032 AL833803 | | AC096032 AL833803 | Kattus no Mus muscu |
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| 36 | | | 180418 | | AC106674 | | AC106674 | Rattus no |
| m | | | 272545 | | AC090533 | | AC090533 | Mus muscu |
| 0 O | - | | 197247 | | AC125713 | | AC125713 | Rattus no |
| 4 | Q | | 261604 | | AC119819 | | AC119819 | Mus muscu |
| 4. | 90.2 | | 168210 | | AC116700 | | AC116700 | Mus muscu |
| 2 4 2 | ۍ ۵ | | 186559 | _ < | AC090495 | | AC090495 | Monse DNA |
| 4 | 89.6 | | 107637 | • | AC094679 | | AC094679 | Rattus no |
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| AUTHOF | | Li, H., Degenha | Degenhardt, | œ m | , Tobin, D., Yao, | Z.X., Tasken,K | n, K. and | |

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BERRRRKAEBEBRRORREBERRRLGKEBERRRREBEBERRRLEBERRRLEBOM
OQIMAALNSOTAVOFQOYAAQOYFQRVEDOOTLITROLOEODHYOOYMOGLYOVQLAAQO
AALGKOGEVVAMAGASLDASSKVNTAGASDTLSVNGQAKTHTRENSEKVLEPERAEBELE
NGPKDSLPVIAAPSMWTRPOIKDFRKEKIRQDADSVITVRRGEVVTVRVPTHEEGSYLE
NGPKDSLPVIAAPSMWTRPOIKDFRKEKIRQDADSVITVRRGEVYTVRVPTHEEGSYLE
LDETYDVYRRDCHEVYREMANSWANSVHVSESSDEBEBEBERWTCEBRAKRNANKPL
LDETYDVARROCHEVYRENGARQYPGRGVYLKFDNSYSLMRSKSVYTRFT
310 C 312 L
                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAB71197.2"
/db_xref="G1:7545291"
/translation="MRKFRCRRAEVRVKDGKAFHPTYEEKLKFVALHKQVLLGPYNPD
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                                                                    2 (bases 736 to 1290)
Li, H. and Papadopoulos, V.
Direct Submission
Submitted (03-SEP-1997) Department of Cell Biology, Georgetown
University Medical Center, 3900 Reservoir Rd. NW, Washington, DC
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Li,H. and Papadopoulos,V.
Direct Submission
Submitted (12-APR-2000) Department of Cell Biology, Georgetown University Medical Center, 3900 Reservoir Rd. NW, Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 156
Identification, localization, and function in steroidogenesis
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                                                                                                                                                                                                                      quence update by submitter
Apr 12, 2000 this sequence version replaced gi:2432020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 1543;
          PAP7: a peripheral-type benzodiazepine receptor- and PKA (RIalpha)-associated protein Mol. Endocrinol. 15 (12), 2211-2228 (2001) 21588728
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                                                                                                                                                                                                                                                                                                                                                    /note="PBR associated protein; PAP7"
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Pred. No. 0;
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                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                               /strain="BALB/c"
/db_xref="taxon:10090"
1. .1543
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99.0%;
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/gene="Pap7"
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                    TCTCATCCGCCAGCTGCAGGAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGGAAA
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                                                                       GAGGCTTCGGCTGGAACAGCAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGC
                                                                                          CCÁACCTGCACAACAACAGGCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGGGC
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PRI 29-SEP-2000

linear

mRNA

2140 bp

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/translation="MAAVLNAERLEVSVOGLTLSPDPEERPGAEGAPLLPPPLPPSP
PGSGROGAGASGERDPEGEAAAGGAABERRLEGGWGFGLELELSLELEFEKEKOGKAF
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FVKLLNRCCHLFSTYVASHKIEKEEODKKRKEEEERRRREEBERRLOKEEEKRREE
FERLRREEBERRRIEBERRRIEBERRRLEGOOKOOIMAALNSGTRNOFGOOTS
IROHOGOYVOGYMQQLYOQUAAGLOKOOLAGOOSTALOKOOYPGWTDSOOTI
GOOAKTHTDSSEKELEPEAAEGALGNOGAACJOKOSLAFFSSKWHWSY
NGOAKTHTDSSEKELEPEAAEGALENOFKESLLVIAAPSNMTRPQINDFKEKTOQODD
                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:odnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                         Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Ashibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVITVGRGEVVTVRVPTHEEGSYLFWEFATDNYDIGFGVYFEWTDSPNTAVSVHVSES
SDDDEEEEENIGCEEKAKKNANKPLLDEIVPVYRRDCHEEVYAGSHQYPGRGVYLLKF
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Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
                                                                                                        clone_lib:HEP
                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, S' - & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                        mRNA,
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Pred. No. 5e-264;
); Mismatches 174; Indels
             fis, clone HEP02419
                                                                                                      t
                                                                          oligo capping; fis (full insert sequence).
Homo sapiens hepatoma cell_line:HepG2 cDNA
clone:HEPO2419.
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/cell_type="hepatoma"
/clone_lib="HEP"
/note="cloning vector pME18SFL3"
49. .1635
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/db_xref="G1:10438061"
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Homo sapiens cDNA: FLJ21867
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ilarity 87.2%;
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2 (bases 1 to 2140)
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NGQAKTHTDSSEKELEPEABEALENDFKESLPVIAAPSNMTRPQIRDFKEKUQDAD
SVITVGRGEVVYPYPPHEEGSYLFWERATDNYDIGFGYYFBWTDSPYRAVSSS
SDDDBEEEENIGCEEKAKKNANKPLLDEIVPVYRRDCHEEVYAGSHQYPGRGVYLKF
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                                                                                                                                           AB043587 3598 bp mRNA linear PRI 28-NOV-2001
Homo sapiens gcp60 mRNA for golgi resident protein GCP60, complete
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                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                               Identification and characterization of a novel Golgi protein, GCP60, that interacts with the integral membrane protein giantin 1576.278
AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 156
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                                                                                                                                                                                                                                                                                       Sohda,M., Misumi,Y., Yamamoto,A., Yano,A., Nakamura,N. and
Ikehara,Y.
                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/protein_id="BAB20592.2"
/db_xref="G1:15799259"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HeCa"
/note="vector:HB814"
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                 TCTCATCCGCCAGCTGCAGGAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAAC
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                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-JUL-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 21 Row: c Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.
Richards, S., Gibbs, R.A.
                                                                                                                1416
 complex associated protein
                GCGGTCAAAATCAGTCTACTAGTCTATTATAATAGTAAAAAATGTTGTTACAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/The
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Baylor College of Medicine Human Genome
Sequencing Center
                                                      CCACCAGTATCCAGGGGGGGGGGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTG
                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                     JO49 bp mRNA linear Homo sapiens, Similar to golgi complex associated kDa, Clone IMAGE:3858463, mRNA, partial cds.
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/tissue_type="Ovary, adenocarcinoma"
/clone_lib="NIH_MGC_66"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://mgc.nci.nih.gov
                                                                                                                                                                     /note="Vector: pCMV-SPORT6"
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60 kDa"
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/db_xref="G1:21961497"
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Contact: MGC help desk
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KEEEKRRREEEERLRREEEERRIEEERLRLEQQKQQIMAALNSQTAVQFQQYAAQQY
PGNYEQQQILIRQLQEQHYQQYMQQLYQQVQLAQQQAALQKQQEVVVA6SSLEPTSSKVN
YPSONMSVNGQAKTHTOSSEKELEPEAAEERLENGFKESLPVIAAPSMWTRQIKD
FKRKIQQAADSVITVRGGEVVTVRPTHEEGSYLFWEFATDNYDIGFGVYFFWTDSPN
TAVSVHVSESSDDDEEEEENIGCEEKAKRNANKPLLDEIVPVYRROCHEEVYAGSHQY
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Pred. No. 8.1e-216;
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15039 CCTTTAGACTCTCTTCCAGTGATTGCAGCTCCATCCATGTGGACAAGACCACAAATCAAA 15098
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CLGSGASGQQREPGEAAAEGAAEEARRMEQHWGFGLEELYGLALRFYKIKDGKAFHPT
SEKLKFYALHKQULLGPYNPDTSPEVGFFDVLGDRRREWALGNWSREDAWYBFVK
LLNKCCPLLSAYVASHRIEKEEERRRAREEERRRAREEERRLGKEEERRREFEDA
LRREEEERRRIEEERRRLEGOKQQIMAALNSOTAVQFOQYAAQQYPGNYEQOQILIRQ
LQCGQYYQQLYQYQLAQQQAALOKQCBVWAGASLPASSKVNTAGASDTLSVNG
AKTHTENSEKVLEPEAAEALBWGFNSLPVIAAPSWWTRPQIKDFKEKIRQDADSVI
TVRRGEVYTVRYPTHEGSSYLEWREFATDSYDIGFGYYFEWTDSPNAAVSVHYSESSDE
EEEEEENVTCEEKAAKNANRPLLDEIVPVYRRDCHEEVYAGSHQYFGRGVYLLKFDNS
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Liu,J. and Papdopoulos,V.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="peripherial benzodiazepine receptor associated protein PAP7"
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.15330,16955. .17228)
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AAAAGAACGCCAACAAGCCTCTGCTGGATGAGATTGTACCTGTGTACCGGCGGGACTGTC 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-APR-2002) Department of Cell Biology, Georgetown University Medical Center, 3900 Reservoir Rd. NW, Washington, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                  DB 10; Length 18140;
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10857. .11031,13325. .13511,15046.
/gene="Pap7"
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10857. .11031,13325. .13511,15046.
/gene="Pap7"
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Pred. No. 4.2e-62;
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/organism="Mus musculus"
/strain="BALB/c"
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/db_xref="G1:20453989"
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1255. .17228
/gene="Pap7"
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Center: Whitehead Institute/ MIT Center for Genome Research
ACAGACAGTTATGACATTGGGGTTTATTTTGAATGGACAGACTCTCCAAATGCT
                                                                 1016 GTCGTCACCGTCCGAGTCCCGACTCATGAGGAAGGATCATACCTATTTTGGGAATTTGCC
                                                                                                                                                                                                                  1136 GCTGTCAGTGTGCATGTCAGTGAGTCCAGTGACGAGGAGGAGGAGGAGGAAG 1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-172B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project Information
Center project name: L23476
Center clone name: 172_B_15
                                                                                                                                                                                                                                                                                                                 AC121292 63971 bp Mus musculus clone RP23-172B15,
                                                                                                                                                                                                                                                                                                                                                AC121292
AC121292.1 GI:20806432
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                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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* NOTE: This record contains 79 individual

896 CCAAAAGACTCTCTTCCAGTGATTGCAGCTCCATCCATGTGGACAAGACCACAAATCAAA 955

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us-09-762-594-2.rge

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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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12887: contig of 700 bp in length
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13698; contig of 711 bp in length
13798; gap of 100 bp
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1 (bases 1 to 140409)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 1, clone RP11-275114
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                  33782 ATCCAGGGAGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTGGAGGTCCA 33841
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55160 55872: contig of 713 bp in length 55873 55972: gap of 100 bp
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Pred. No. 1.3e-51;
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AC044825.2 GI:9502452
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens.
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------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                             1.00182149362477Chemistry: Dye-terminator Big Dye; 100% of
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                               M13; M77815; 99% of reads
Plasmid; n/a; %-0.f%% of reads
                                                         Consensus quality: 120391 bases at least Q40 Consensus quality: 129577 bases at least Q30 Consensus quality: 133768 bases at least Q30 Insert size: 160000; agarose-fp Insert size: 136609; sum-of-contigs Quality coverage: 3.1 in Q20 bases; agarose-fp Quality co.
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of 1169 bp in length
100 bp
of 2422 bp in length
100 bp
of 1128 bp in length
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of 1009 bp in length
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25903: contig of 2667 bp in length
26003: gap of 100 bp
29651: contig of 3648 bp in length
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f 1211 bp in length
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of 1714 bp in length
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contig of 1478 bp in length
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35597: contig of 2496 bp in length
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contig of 3250 bp in length
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                                                                                                                                                                                                                                                                                         Assembly program: Phrap; version 0.960731
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1257 2265: contig of
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19331: cont
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23136: cont
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misc_feature

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49423: gap of 100 bp
52514: contig of 3091 bp in length
52614: gap of 100 bp
56594: contig of 3980 bp in length
                                                  100 bp
3646 bp in length
                                                                       p of 100 bp
contig of 4053 bp in length
                                                                                          93: gap of 100 bp 68645: contig of 4052 bp in length
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hote="assembly_fragment"
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hote="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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0510. .11838
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note="assembly_fragment"
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note="assembly_fragment"
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/db_xref="taxon:9606"
                                                56694: gap of 1
60340: contig of
49323: contig of
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71501: cont
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HTG 17-AUG-2002
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                                                                                                                                                                                           896 CCAAAAGACTCTTCCAGTGATTGCAGCTCCATCTGGACAAGACCACAAATCAAA 955
                                                                                                                                                                                                                                                                                                GTCGTCACCGTCCCGAGTCCCGACTCATGAGGAAGGATCATACCTATTTGGGAATTTGCC
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                         Length 140409;
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Sequencing vector: M13; M77815; 0% of reads
Sequencing vector: plasmid; L08752; 99% of reads
Chemistry: Dye-primer-amersham; 0% of reads
Chemistry: Dye-terminator; 9% of reads
                                                                                                                                         Score 238; DB 2; I
Pred. No. 1.7e-49;
0; Mismatches 50;
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                                 35698. 37964
/note="assembly_fragment"
38065. 41070
/note="assembly_fragment"
41171. 43345
/note="assembly_fragment"
43446. 46364
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/note="assembly_fragment"
35698. .37964
/note="assembly_fragment"
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Best Local Similarity 84.3%;
Matches 268; Conservative
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AL592045/c
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         HTG; HTGS_PHASE1
                                            Homo sapiens
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AC021883.4 GI:9910096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DD 104979 GTGGTCACTGTTCGAGTACCCACCCATGAAGGATCATATCTCTTTTGGGAATTTGCC 104920
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Chemistry: Dye-terminator ET-amersham, 0% of reads Chemistry: Dye-terminator Big Dye: 90% of reads consensus quality: 181214 bases at least Q40 Consensus quality: 18143 bases at least Q30 Consensus quality: 181535 bases at least Q20 Insert size: 181619; sum-of-contigs Insert size: 184421; 3.1% error; agarose-fp Quality coverage: 12.97x in Q20 bases; sum-of-contigs Quality coverage: 13.26x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 181719;
                                                                                                                                                                                                                                                                                                                                            179558 199557: contig of 179557 bp in length 179558 199557: gap of 100 bp 179558 181719: contig of 2062 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 others
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Pred. No. 1.7e-49;
0; Mismatches 50;
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42290 c 42015 g 47265 t
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clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .179557
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179658. .181719
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84.3%;
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Direct Submission (21-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                       Aug 25, 2000 this sequence version replaced gi:9838290
                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13: 86%
Sequencing vector: plasmary Statistics
Sequencing vector: plasmaid; 14%
Chemistry: Dye-primer ET; 86% of reads
Chemistry: Dye-terminator Big Dye; 14% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 211796 bases at least Q40
Consensus quality: 217990 bases at least Q20
Insert size: 181000; agazose-fp
Insert size: 228280; sum-of-contigs
Quality coverage: 6.35 in Q20 bases; gaarose-fp
Quality coverage: 6.35 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
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Waterston, R.H.
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9290:
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unknown

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ig of 20766 bp in length of unknown length g of 27290 to
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g of 2368 bp in length
if unknown length
of 4462 bp in length
of unknown length
g of 4054 bp in length
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g of 4253 bp in length
if unknown length
of 0659 bp in length
of unknown length
g of 8745 bp in length
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Location/Qualifiers
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of 31058 bp in length
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/note="assembly_name:Contig15"
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/db_xref="taxon:9606"
/chromosome="1"
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        GCTGTCAGTGGCATGTCAGTGAGTCCAGTGAGGAGGAGGAGGAGGAAGAAATGTC
        1195

        DD
        178689
        GCTGTCAGCGTGCATGTCAGTGAGTCCAGCGATGACGAGGAGGAAGAAGGTAGAACC
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18152. 1935an017_numme.contigory
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31869. 337868
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5027. .25594

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52695. .57156

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40442. .42574
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42675. .44938
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45039. .50126
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Llarity 84.3%; Pred. No. 1.8e-49;
Conservative 0; Mismatches 50
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft" sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Baylor Plaza, Houston, TX 77030, USA
On Jul 7, 2002 this sequence version replaced gi:21699099.
                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
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Consensus quality: 107819 bases at least Q40
Consensus quality: 114791 bases at least Q30
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                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Rightooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,

Rlabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,

Barbaria, J., Benton, J. Binage, K.C., Blankenburg, K., Bonnin, D.,

Bunay, C., Burch, P., Briekelt, C., Burch, R., Byrd, N.C.,

Carron, T.F., Carter, M., Cavazos, S.R., Clacko, J., Chavez, D.,

Carron, T.F., Carter, M., Cavazos, S.R., Clacko, J., Chavez, D.,

Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,

Cleveland, C.D., Cox, C., Coyole, M.D., Dathorne, S.R., David, R.,

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Hansis, A., Gao, J., Carcia, A., Ganer, T., Garza, N., Gill, R.,

Gorrell, J.H., Guevara, M., Gunzatane, P., Hale, S., Hannadez, J.,

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Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Mayen, M., Morter, M., Nauyen, N.,

Mapus, M., Wabuu, P., Martin, R., Martinez, M., Mayhue, K., Werden, S., Watcher, W., Nauyen, N.,

Mayen, M., Nedla, D., Newtson, J., Nauyen, M., Weyden, N.,

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Scherers, S., Scott, G., Shen, W., Stanon, J.,

Sodergren, S., Soraike, T., Sparks, A., Stanley, H., Tang, H.,

Sodergren, S., Soraike, T., Sparks, A., Stanley, H., Wooden, S., Watlians, G., Walliams, G.,

Walliams, G., Williams, G., and Gibbs, R.,

Direct, Submission
                                                                                                                                                                  Rattus norvegicus clone CH230-162N10, *** SEQUENCING IN PROGRESS
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of Molecular and Human Genetics, Baylor College of Medicine, One
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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2235 bp mRNA linear Homo sapiens cDNA FLJ32556 Fis, clone SPLEN1000134. AK057118

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GTCCGTCTACTACAGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTCC 1425

Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

oligo capping; fis (full insert sequence). Homo sapiens spleen cDNA to mRNA, clone_lib:SPLEN1 clone:SPLEN1000134.

Homo sapiens

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Submitted (24-007-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics&hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan KRY Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
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Rawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishli, S., Yamamoto, J.,
Isono, Y., Kawai-Hio, Y., Salto, K., Nishlkawa, T., Kimura, K.,
Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H.,
Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
Marahashi, Puji, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahari, K.,
Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
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Pred. No. 7.2e-43;
); Mismatches 36
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Direct Submission
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/db_xref="taxon:9606"
/clone="splen1000134"
/tissue_type="spleen"
/clone_lib="spleen"
/note="cloning_vector: pME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 7030, USA on Jul 7, 2002 this sequence version replaced g1:21699099.

Center: Baylor College of Medicine
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                         1306 TCCAGGGAGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTCTGTGGAGGTCCAA 1365
                                                      1656 TCCAGGGAGAGGAGTCTATCTCCTCAAGTTTGACAACTCCTACTCTTTGTGGCGGTCAAA 1715
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                                                                                                                                                         1337 GATAATTCCTACTCTCTGTGGAGGTCCAAGTCCGTCTACTACAGAGTCTATTATACTAGA 1396
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AK095650 3547 bp mRNA linear PRI 15-JUL-2002 Homo sapiens CDNA FLJ3831 fis, clone FCBBF3025285, moderately similar to Mus musculus peripherial benzodiazepine receptor
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                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,
Sugiyana, T., Iffe, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A.,
Ishii, S., Yamamoto, J., Isono, Y., Kawai, Hio, Y., Saito, K.,
Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi Fujii, A., Oshima, A.,
Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K.,
Masuho, Y., Nagai, K. and Isogai, T.
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                              oligo capping; fis (full insert sequence).
Homo sapiens fetal brain cDNA to mRNA, clone_lib:FCBBF3
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/db_xref="taxon:9606"
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associated protein (Pap7) mRNA
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/note="cloning vec
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Isogai, T. and Yamamoto, J.
Direct Submission
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TDITVQVSDSSDDEDEEEEEEEEEEEFPVPAGDVERGSRSSLRGRYGEVMPVYRRDSHR
DVQAGSHDYPGEGITLLKFDNSYSLLRKTLYFHIXYTS"
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Mang,J.R., Zhao,Q.A., Wang,D., Liu,C., Drmanac,R.T. and Wehrman,T.
Nucleic acids and polypeptides
Patent: WO 0218424-A 238 07-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1232 CCTCTGCTGGATGAGATTGTACCTGTGTACCGGGGGACTGTCACGAGGAAGTATATGCA 1291
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1. .882
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109. .882
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